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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

July 25, 2004, 09:54:25; Search time 987 Seconds (without alignments) 7503.317 Million cell updates/sec Run on:

US-10-690-617-1_COPY_173_1687 Title: Perfect score:

1 atggaggggggtccagctgt.....aggaagacgaggctgcatcc 1515 IDENTITY NUC Sequence:

Gapop 10.0 , Gapext 1.0 Scoring table:

3216467 seqs, 2444149694 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

6432934

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

Published Applications NA:*

1: cgn2 6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: cgn2 6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
3: cgn2 6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
4: cgn2 6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
5: cgn2 6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
6: cgn2 6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
7: cgn2 6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
8: cgn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: cgn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: cgn2 6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: cgn2 6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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18: cgn2 6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
19: cgn2 6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: cgn2 6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: cgn2 6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
19: cgn2 6/ptodata/1/pubpna/USO0_NEW PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli	Sequence 1, Appli	Sequence 39, Appl		Sequence 55, Appl	Sequence 9, Appli	Sequence 43, Appl	Sequence 7, Appli	Sequence 41, Appl	Sequence 14, Appl	Sequence 53, Appl	Sequence 57, Appl	Sequence 7, Appli	Sequence 8, Appli
αı	US-10-135-689-1	US-10-690-617-1	US-10-333-314-39	US-10-302-172-433	US-10-092-900A-55	US-09-922-138-9	US-10-391-364-43	US-09-922-138-7	US-10-391-364-41	US-10-168-582-14	US-10-092-900A-53	US-10-092-900A-57	US-10-316-124-7	US-10-316-124-8
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* Query Match Length DB	2190	2190	1937	2018	1611	1683	1686	2711	2711	3501	1547	1725	4427	4427
% Query Match	100.0	100.0	99.7		99.4									
Score	1515	1515	3 1510.2	1507	(5) 1505.4	1490.6	1490.6	1490.6	1490.6	1457.2	1455.8	1381.4	-651.2	651.2
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51,	Z,	금	Sequence 22, Appl	225	e 183	20	23	e,	Sequence 3, Appli	84	24	16	12	2684	2780	Sequence 5606, Ap	Sequence 22375, A	Sequence 1008, Ap	Sequence 1603, Ap	Sequence 1603, Ap	Sequence 1603, Ap	92	19	Sequence 192, App	Sequence 1333, Ap	Sequence 1390, Ap	Sequence 15808, A	Sequence 33104, A	5993	
US-10-205-823-	5 US-10-205-823-53	6 US-10-295-027-1	US-10-098-841-2	60-SN	-764 - 875 - 1	.296-115-2	14 US-10-098-841-23	14 US-10-135-689-3	17 US-10-690-617-3	17 US-10-283-975A-847	13 US-10-296-115-247	13 US-09-823-245A-163	10 US-09-918-995-1271	13 US-10-425-114-26840	10 US-09-918-995-2780	9 US-09-864-761-5606	9 US-09-864-761-22375	16 US-10-305-720-1008	9 US-09-764-869-1603	15 US-10-091-504-1603	7-577-1	9 US-09-764-869-192	15 US-10-091-504-192	-19	-09-954-456-133	9 US-09-880-107-1390	US-10-425-114	0-425-114-331	US-10-437-963-599	13 US-10-425-114-3580
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ALIGNMENTS

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Sequence 1, Application US/10135689

Publication No. US20020123121A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION WUMBER: US/10/135,689

CURRENT FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: 60/247,031

PRIOR APPLICATION NUMBER: 09/729,995

PRIOR FILING DATE: 2000-11-3

PRIOR FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 4.0
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Matches 1515; Conservative
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CRGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: INVIE GENOMICS, INC.; YUE, Henry
APPLICANT: HARALIA, April J.A.; CHAMLA, Narinder K.
APPLICANT: HARALIA, April J.A.; CHAMLA, Narinder K.
APPLICANT: ARAVIZU, Chandra S.; RAMKUMAR, Jayalaxmi,
APPLICANT: GANDHI, Amena R.; POLICKY, Jennifer L.
APPLICANT: BAUGHN, Mariah R.; FIRIBOULEY, Catherine M.
APPLICANT: THORNION, Michael B.; BANDMAN, Olga
APPLICANT: THORNION, Michael B.; LU, Yan
APPLICANT: BUREORD, Neil; LAL, Preeti G.
APPLICANT: BUREORD, Neil; LAL, Preeti G.
APPLICANT: BUREORD, Neil; LAL, Preeti G.
APPLICANT: BUREORD, Ji YAO, Monique B.
APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
APPLICANT: GREENWALD, Sara R.; TANG, Junming
APPLICANT: GREENWALD, Jennifer L.
APPLICANT: GREENWALD, Jennifer L.
APPLICANT: JACKSON, Jennifer L.
APPLICANT: JACKSON, Jennifer L.
APPLICANT: GIETZEN, Kimberly J.; YANG, Junming
APPLICANT: JACKSON, Jennifer L.
APPLICANT: BAPLICATION NUMBER: US 60/220,038
FRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-09-04
PRIOR PRI
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99.8%; Pred. No. 0;
tive 0; Mismatches
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b; OTHER INFORMATION: Incyte ID No: 2190612CB1
US:10-333-314-39
                                                                                                                                                                                                                                                                             US-10-333-314-39
. Sequence 39, Application US/10333314
. Publication No. US20030211093A1
. GENERAL INFORMATION:
                                                                                                                                                  1673 GACGAGGCTGCATCC 1687
                                                                                                                     GACGAGGCTGCATCC 1515
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Best Local Similarity 99.8
Matches 1512; Conservative
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ORGANISM: Homo sapiens
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US-09-202-138-9
| US-09-202-138-9
| Sequence 9, Application US/09922138
| Patent No. US20020061574A1
| GENERAL INFORMATION:
| APPLICANT: Milennium Pharmaceuticals, Inc.
| APPLICANT: Milensium NOVEL HUMAN |
| TITLE OF INVENTION: 16658, 14223, AND 16002, NOVEL HUMAN |
| TITLE OF INVENTION: 16658, 14223, AND 16502, ISS |
| CURRENT APPLICATION NUMBER: US 60/9922, ISS |
| PRIOR APPLICATION NUMBER: US 60/229, 299 |
| PRIOR PILING DATE: 2000-09-01 |
| NUMBER OF SEQ ID NOS: 38 |
| SOOFTHARE: FASEUED for Windows Version 4.0
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Best Local Similarity 99.4
Matches 1496; Conservative
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TYPE: DNA
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                                                                                                                                                                       Score 1505.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                        99.4%;
                                                                                                                                                                       Query Match
Best Local Similarity 99.6
Matches 1509; Conservative
 768
                                                TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                 ; NAME/KEY: CDS
; LOCATION: (52)..(1567)
US-10-092-900A-55
NUMBER OF SEQ ID
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LENGTH: 1611
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	RESULT 7 US-10-391-564-43 US-10-391-564-43 US-10-391-564 US-10
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                       901 GAGGGGAACGACGCTCAGCTGTCCAGCACGGGGGGAACCCCCAGCATTCATGGCCCCCGAG
                                                                 GCCATTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC
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Sequence 7, Application US/09922138
Setent No. US20020061574A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
FILE OF INVENTION: 16658, 14223, AND 16002, NOVEL HUMAN
TITLE OF INVENTION: 16658, 14223, AND 16002, CURRENT APPLICATION NUMBER: US/09/922,138
CURRENT FILING DATE: 2000-11-28
PRIOR PAPLICATION NUMBER: US 60/229,299
PRIOR FILING DATE: 2000-01
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 2711
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ORGANISM: Homo sapiens
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llarity 99.4%; Pred. No. 0;
Conservative 0; Mismatches
SEQ ID NO 43
LENGTH: 1686
TYPE: DNA
ORGANISM: HOMO SADIENS
FRATURE:
                                                                                            ... (1686)
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Best Local Similarity
Matches 1496; Conserv
                                                                           ; NAME/KEY: CDS
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US-10-391-364-43
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APPLICANT: Meyers, Rachel E.
APPLICANT: Carroll' Joseph M.
APPLICANT: Carroll' Joseph M.
APPLICANT: Cock, William James
APPLICANT: Cock, William James
APPLICANT: Rapeller-Libermann, Rosana
APPLICANT: Rapeller-Libermann, Rosana
APPLICANT: Meich, Nadine S.
TITLE OF INVENTION: NOVEL 27877, 18080, 1408:
TITLE OF INVENTION: NOVEL 27877, 18080, 1408:
TITLE OF INVENTION: 16658, 14223, 16002, 500;
TITLE OF INVENTION: 1658, 14002, 500;
TITLE OF INVENTION: 1658, 14002, 500;
PRIOR PELICATION NUMBER: US 60/231, 084
PRIOR FILING DATE: 2001-11-13
PRIOR PELICATION NUMBER: US 60/338, 587
PRIOR FILING DATE: 2001-11-13
PRIOR PELICATION NUMBER: US 60/328, 198
PRIOR PELICATION NUMBER: US 60/328, 198
PRIOR PELICATION NUMBER: US 60/314, 707
PRIOR PELING DATE: 2000-11-21
PRIOR PELING DATE: 2000-06-27
PRIOR PELING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 41, Application US/10391364; Publication No. US20040121349A1; GENERAL INFORMATION:
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JOS-10-168582

Publication No. US20040058426A1

GENERAL INFORMATION:

APPLICANT: NUCYTE GENOMICS, INC.

APPLICANT: BAUGHN, Mariah R.

APPLICANT: BURFORD, Noil

APPLICANT: BURFORD, Noil

APPLICANT: AU-YOUNG, Janice

APPLICANT: REDDY, Roopa

APPLICANT: REDDY, Roopa

APPLICANT: YUE, Henry

APPLICANT: YAO, Wonique G.

APPLICANT: YAO, Wonique G.

APPLICANT: KAAN, Farrah A.

ITLER ERFERENCE: PI-0002 PCT

CURRENT APPLICATION NUMBER: US/10/168,582
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PRIOR APPLICATION NUMBER: US 60/327,820
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SCOFTWARE: Factor of Windows Version 4.0
SEQ ID NO 41
LENGTH: 2711
TYPE: DNA
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Matches 1496; Conservative
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Shency, Suresh G.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Li, Li, Li, Li, APPLICANT: Li, Li, Li, Li, APPLICANT: Carbusen, Bryan D.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Ji, Weizhen
APPLICANT: Grman, Linda
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Rekuda, Ramesh
APPLICANT: Gangolli, Esha A.
APPLICANT: Gangolli, Esha A.
APPLICANT: Geo, Xiaojia Sasha
APPLICANT: Tchernev, Velizar T.
APPLICANT: Fernandes, Elma R.
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CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731
PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
NUMBER OS SEQ ID NOS: 24
SOFTWARE: PERL PROGRAM
SEQ ID NO 14
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; OTHER INFORMATION: Incyte ID No. US20040058426A1 2041716CB1
US-10-168-582-14
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Pred. No. 0;
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Best Local Similarity 97.9%;
Matches 1509; Conservative 0
                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                             LENGTH: 3501
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J. 10. 11. 12. 13. 14. 15. 16. 17. 18. 18. 18. 18. 18. 18. 18	11ILE CFINTALION: NO: 022004004338ZAATE1 FIOLEIUS AND NUCLEIC ACIDS ENCOALING SANNE; CURRENT APPLICATION NUMBER: US/10/092,900A CURRENT FILING DATE: 2002-03-07 PRIOR APPLICATION NUMBER: USSN 60/274,322 PRIOR PILING DATE: 2001-03-08 PRIOR PILING DATE: 2001-03-08 PRIOR PILING DATE: 2001-04-13 PRIOR APPLICATION NUMBER: USSN 60/283,675 PRIOR PILING DATE: 2001-04-13	PRIOR FILING DATE: 2001-12-03 PRIOR APPLICATION NUMBER: USSN 60/274,281 PRIOR PILING DATE: 2001-08-08 PRIOR PILING DATE: 2001-03-08 PRIOR PILING DATE: 2001-03-08 PRIOR FILING DATE: 2001-03-08 PRIOR PILING DATE: 2001-09-27 PRIOR PILING DATE: 2001-09-27 PRIOR PILING DATE: 2001-09-27 PRIOR PILING DATE: 2001-07-10	PRIOR APPLICATION NUMBER: USSN 60/279,995 ; PRIOR FILING DATE: 2001-03-30 ; PRIOR FILING DATE: 2001-05-31 ; PRIOR PILING DATE: 2001-05-31 ; PRIOR PILING DATE: 2001-05-31 ; PRIOR FILING DATE: 2001-04-30 ; Remaining Prior Application data removed - See File Wrapper or PALM.) NUMBER OF SEQ ID NOS: 768 ; LENGTH: 1547 ; TYPE: DNA ; TYPE: DNA ; TYPE: DNA	DOMESTICAL DESCRIPTION (20)(1529) LOCATION: (20)(1529) LOCATION: (20)(1529) LOCATION: (20)(1529) LOCATION: (20)(1529) Query Match Query Match 96.1%; Score 1455.8; DB 13; Length 1547; Query Match 98.5%; Pred. No. 0; Matches 1492; Conservative 0; Mismatches 17; Indels 6; Gaps Matches 1492; Conservative 1; Indels 1; Indels 1; Indels 1; Indels 1; Indels 1; Indels 2; Gaps 1 ATGGAGGGGGGTCCAGGTGTCTGCTGCAGGATCCTCGGGCAGAGCTGTAGAAACGGGT	ACCAGAGE 3 ACCAGAGE 1 ACCAGAGE 1 TCAAGA 1 TCAAGA 1 TCAAGA 1 TCAAGA 1 TCAAGA 2 CCAGCA 2 CCAGCA 2 ATCTCC 3 ATCTCC 3

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                                                                                                                                                                                                                   Best_Local Similarity 92.6
Matches 1509, Conservative
                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                       ) NAME/KEY: CDS
; LOCATION: (52)..(1681)
US-10-092-900A-57
SEQ ID NO 57
LENGTH: 1725
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APPLICANT: Catterton, Elina
APPLICANT: Leite, Mario W.
APPLICANT: Leite, Mario W.
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: NO. US20400043382Alel Proteins and Nucleic Acids Encoding Same FILE REPERBYCE: 21402-2907
CURRENT FILIAG DATE: 2002-03-07
FRICH REPERBYCE: 2001-03-08
FRICH REPERBYCE: 2001-03-08
FRICH REPERBYCE: 2001-03-08
FRICH REPERBYCE: 2001-04-13
FRICH REPERBYCE: 2001-04-13
FRICH REPERBYCE: 2001-04-13
FRICH REPERBYCE: 2001-03-08
FRICH REPERBYCE: 2001-03-30
FRICH APPLICATION NUMBER: USSN 60/279,995
FRICH RELING DATE: 2001-03-30
                                                                       AACCCGITTGAGCCCCCAAGCACGGAGGBAAGAGCGATCCATGTCTGCTCCAGGAAACCTA 1453
                                          CTGGTGAAAGAAGGGTTTTGGTGAAGGGGGCAAGAGCCCCAGAGCTCCCCGGCGTCCAGGAA
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PRIOR APPLICATION NUMBER: USSN 60/287,424
PRIOR FILING DATE: 2001-04-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 768
                                                                                                                                                                                                                                                                             Sequence 57, Application US/10092900A Publication No. US20040043382A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     Spytek, Kimberly A.
Shenoy, Suresh G.
Taupier Jr., Raymond J.
Pena, Carol E.A.
Li, Li
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
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Tchernev,, Velizar T.
Fernandes, Elma R.
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Zerhusen, Bryan D.
Gusev, Vladimir Y.
Ji, Weizhen
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Gangolli, Esha A.
Vernet, Corine A.M.
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Malyankar, Uriel M.
Gerlach, Valerie
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Spaderna, Steven K.
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Miller, Charles E.
Kekuda, Ramesh
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                                                                       Length
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Pred. No. 4.3e-181;
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Sequence 7, Application US/10316124

Publication No. US20030152574A1

APPLICANT: Logan, Thomas Joseph
APPLICANT: Logan, Thomas Joseph
TILLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
TILLE OF INVENTION: MATHODS AND COMPOSITIONS TO TREAT
TILLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
FILE REFERENCE: MPIO1-291PIRM
CURRENT APPLICATION NUMBER: US/10/316,124

CURRENT FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: 60/339,995

PRIOR FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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DD 720 CAATGTGGTGAAGGTCCTGGATGACCCCAATGAGGACCATTGTACATGGT 779	1167 GTTAGACAAGAATCCCGAGACATTGGGGTGCCAGACATCAAGTTGCACCCTTGGGT 1226	1347 GGTGAAGTCCATGCAGAACTTTGGAAACCGTTTGGCAACCGTGATCCTTTGGAACCCTTGGCAACCGTGATCCTTTGGAACCCGTTTGGGAACCGTTTGGGAACCGTTTGGGAACCGTTTGGGAACCGTTTGGGAACCGTTTGGGAGGCACCGGGGGGGG	RESULT 15 US-10-205-823-51 Sequence 51, Application US/10205823 Publication OS US20030108963A1 Publication No. US20030108963A1 APPLICANT: Monhan, John E. APPLICANT: Bndege, Wilson O. APPLICANT: Gannavarapu, Manjula APPLICANT: Gannavarapu, Manjula APPLICANT: Gansech, Sebastian APPLICANT: Kamackar, Shubhangi APPLICANT: Wonsey, Angela M. APPLICANT: Wonsey, Angela M. APPLICANT: Glatt, Karen
OY 1287 GACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTGGACCACGGGATCT 1346 Db 1380 GACTGAAGAGGAGGTCAAACACAGTCAAACACATTCCCAGCTGGCAACCGTGATCT 1439 OY 1347 GGTGAAGACTCAGCTGAAACACATTCCTAGGCACCAGCACGAGG 1406 Db 1440 GGTGAAGACCATGATACGTAAACGCTCTTTGGGAACCCTTTCAGGCCCCAGCACGAGG 1406 OY 1407 GGTGAAGACCATGATACGTAAACGCTCTTTGGGAACCCATTCGAGGGCAGCCGGCG 1406 OY 1407 GGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTCGAGGGATG 1556 OY 1407 GGAGAAGACCATGATACGTAAACGCTCCTTTGGGAACCAACACAGGGAATG 1556 OY 1407 GGAGAAGACCATGATCATGCTCCAGGAAACTTGCTCACCAAAAACCAACC	70 8 II. 4427 DNA SM. Homo sapiens EE: EX. CDS CON: (127)(1653) 124-8 A1.08; Score 651 ctch a1 Similarity 71.38; Pred. No.		A17 TGAAGACAGACACTATGCAATGAAAGTCCTTTCCAAAAGAAGTTACTGAAGCAGTATGG 506

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APPLICANT: ZAGO, AUMEN
APPLICANT: ANGERSON, AUMEN
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AUD
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AUD
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-04
CURRENT PREPLICATION NUMBER: US/10/205,823
CURRENT PILING DATE: 2002-07-25
PRIOR PELIANG DATE: 2001-07-25
PRIOR PELIANG DATE: 2001-07-25
PRIOR PELIANG DATE: 2001-09-25
PRIOR PELIANG DATE: 2001-09-25
PRIOR PELIANG DATE: 2001-09-25
PRIOR PELIANG DATE: 2001-12-12
PRIOR PELIANG DATE: 2001-12-12
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Pred. No. 4.5e-181;
0; Mismatches 348;
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Best Local Similarity 71.33
Matches 873; Conservative
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                      1256 CTCTGGGAAGGCCTTGGATGTTTGGGCCATGGGTGTGACACTATACTGCTTTGTCTTTGG
                                                                                                                                                                                     CCAGTGCCCATTCATGGACGACGGGTCATGTGTTTACACAGTAAGATCAAGAGTCAGGC
                                                                                                                                                                                                                                         CGTGGTGTTTCCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGAT
                                                                                                                                                                                                                                                                       1376 CCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAGGACCTGATCACCCGTAT
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  CACGGCGGGAACCCCCAGCATTCATGGCCCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTT
                                                                               CAGTGGGAAGGCCTTGGATGTATGGGCCACTGGCGTCACGTTGTACTGCTTTTGTCTATGG
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us-10-690-617-2.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

(without alignments)
852.223 Million cell updates/sec July 12, 2004, 04:23:48 ; Search time 57 Seconds Run on:

US-10-690-617-2 2634 Perfect score: Title:

505

1 MEGGPAVCCQDPRAELVERV......FGEGGKSPELPGVQEDEAAS

Sequence:

BLOSUM62 Scoring table:

283366 segs, 96191526 residues Gapop 10.0 , Gapext 0.5 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 1.2.6.4 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Ca2+/calmodulin-de	Ca2+/calmodulin-de	calcium/calmodulin	probable Ca2+/calm	serine/threonine-p	protein kinase PAK	serine/threonine-p	probable serine/th	related to protein	probable serine/th	probable serine/th	serine/threonine-s	probable serine/th	probable serine/th	serine/threonine-s	probable serine/th	SNF-related kinase	hypothetical prote	probable protein k	probable protein k	serine/threonine-s	protein kinase (EC	probable serine/th	serine/threonine p	probable protein k	probable serine/th	probable serine/th	serine/threonine-s	probable carbon ca
ID	A57156	JC5669	JE0191	T37317	858666	S50632	T47464	S57252	T51085	T14736	T14735	A56009	T14822	T07788	JC1446	T10449	B90100	E85362	C84667	E84707	T52633	S52242	T18611	T50802	B84644	A86427	T07415	A26030	T41587
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Q Score M	2452	1494	1472.5	1043	620	266	512	507.5	468	448	437	436.5	434	429.5	426.5	423.5	418.5	416.5	415.5	413.5	412.5	410	409.5	409	406.5	406	405.5	403.5	403
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GIN4 protein - yea serine/threonine-s	protein H39E23.1 [probable serine/th	probable serine/th FOG2 protein - yea	protein T25K16.13 myosin-light-chain	probable protein k	Ca2+/calmodulin-de hypothetical prote	protein kinase (EC	p69Eg3 protein - A	SNF1-related prote	serine/threonine-s
S59359 S59941	G89287 T06107	T04862 S72513	G86141	T02306	S43845 T29858	JQ1150 T20941	S52244	S62365	T09903
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403 401	399.5 399	398.5	397	394.5	394.5	394	392	392	391
30	32 33	34 35	36	38	39 40	41	43	44	45

ALIGNMENTS

RESULT 1
A57156
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - rat
N;Alternate names: CaM-kinase kinase; microtubule-associated protein 2 kinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Feb-1996 #sequence revision 23-Feb-1996 #text change 21-Jul-2000
C; Accession: A57156; JC4789
R;Tokumitsu, H.; Enslen, H.; Soderling, T.R.
J. Biol. Chem. 270, 19320-19324, 1995
Affitle: Characterization of a Ca(2+)/calmodulin-dependent protein kinase cascade. Molect
A;Reference number: A57156; MUID:95370263; PMID:7642608
A;Accession: A57156
A;Status: preliminary
A;Molecule type: mRNA

A;Croserer 119, 1176-1181, 1996
A;Title: Evidence for the existence of Ca2+/calmodulin-dependent protein kinase IV kinase.
A;Accession. 119, 1176-1181, 1996
A;Title: Evidence for the existence of Ca2+/calmodulin-dependent protein kinase IV kinase.
A;Reference number: JC4789; MUID:96425004; PMID:8827455
A;Accession. JC4789
A;Residues: 1-44, 'P',46-80,'G',82-505 <OKU>
A;Residues: 1-44,'P',46-80,'G',82-505 <OKU>
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A;Residues: 1-42,'P',46-80,'G',82-505 <OKU>
A;Residues: 1-42,'Region: protein kinase homology kKIN
C;Reywords: ATP; brain; calmodulin binding; phosphotransferase; protein kinase
F;134-142/Region: protein kinase ATP-binding motif

ö Gaps .. Length 505; Query Match 93.1%; Score 2452; DB 2; Length 5 Best Local Similarity 93.1%; Pred. No. 3.3e-101; Matches 470; Conservative 11; Mismatches 24; Indels

1 MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR 60		61 ILPARPSISARKISLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120	61 PTPVRPSLSARKFSLQERPAESCLEAQVGPYSTGPASHMSPRAWRRPTIESHHVALSDTE 120	121 DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ 180	121 DCVINOVKI OSEIGKGAVGVURIA YNEREDRHYAMKVI SKKKII KOVGEPREPPRIGGO 180
MEGGPAVCCODPRAELVERVAAIDVTHLEE	MERSPAVCCODPRAELVERVAAISVAHLEE	LLPARPSLSARKLSLQERPAGSYLEAQAGP	PTPVRPSLSARKFSLQERPAESCLEAQVGP	DCVQLNQYKLQSEIGKGAYGVVRLAYNESE	DCVOL.NOVKT.OSETGKGAVGVVRT.AVNERE
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241 VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300

g ò

Qy 406 HPWVTKNGEEPLPSEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEP 465	A, Reference number: JE0191 A, Molecule type: mRNA A, Residues: 1-417 < HSU> C, Comment: This enzyme functions as a key intermediaries in C C, Genetics: A, Gene: CaMKK A, Map position: 12 C, Superfamily: unassigned Ser/Thr or Tyr-specific protein kir. C, Keywords: phosphotransferase C, Keywords: phosphotransferase F, 47-330/Domain: protein kinase homology < KIN> C, Republic Coal Similarity 68.9%; Score 1472.5; DB 2; Lengt Best Local Similarity 68.9%; Pred. No. 38-58; Matches 272; Conservative 72; Mismatches 50; Indels OP PATGPASHISPRAWRRPTIESHHVAISDAEDCVQLNQYKLQSEIGK OP 11 PYSPVSSPQSSPRIPPRESHYVSITGMQDCVQLNQYTLCABIGK DD 71 DNTYYAMKVLSKKKLIKQYGFPRRPPPRGSQAAQGGPAQCIPERD FINE SIMILATE SIMIL	Db 131 NVKLVEVLIDPRAEHLYNFELVNGSPWENPTILKIENTELFINGTETHING 190 Qy 270 KIVHRDIKPSNILLGDDGHVKIADFGVSPWENPTILKDEDGARFYFODLKGIETHING 190 Db 191 KIIHRDIKPSNILLGDDGHVKIADFGVSNEFKGSDALLSNTVGTPAFMAPESISBEGGSF 329 (A) 330 SGKALDVWATGVTLYCFVYGCPFIDDFILALHRKIKNEPVYPEEPEISEELKDLILKM 389 (B) 251 SGRALDVWATGVTLYCFVYGCPFIDDFILALHRKIKNEPVYPEEPEISEELKDLILKM 310 (C) 330 LDRWPETRIGVDDIKLHPWYTKGEPELPSEELGSVYPTGESVKNSKLIFSWTTVIL 449 (D) 251 SGRALDVWATGVTLYCFVYGCPFIDDFILALHRKIKNEPVYPEGSVKNSKLIFSWTTVIL 449 (D) 310 LDRWPETRIGVDDIKLHPWYTKGEPELPSEELGSVYPTGESVKNSKLIFSWTTVIL 449 (D) 311 LDRWPESRIVVPEIKLHPWYTRGAEPLPSEERECSVYSVRHIFSLATVIL 370 (C) 450 VKSWLRKRSFGNPFE-GSRREERSMSAPGNLLTKK 404 RESULT 4 T37317 Probable Ca2+/calmodulin-dependent protein kinase kinase (EC 2.7.1) - Caenorhabditis (5) percies: Caenorhabditis elegans C, 5pecies: Caenorhabditis elegans C, 5pecies: Caenorhabditis elegans C, 5pecies: Caenorhabditis elegans C, 5pecies: Caenorhabditis elegans C, 5pecesion: T37317 R; Edelman, A.M.; Mitchelhill, K.I.; Selbert, M.A.; Anderson, K.A.; Hook, S.S.; Stapletton J. Baiol. Chem. 271, 10806-10810, 1996
Db 241 VPCDKPFPEEQARLYLEDIIGALEYLHCOKIVHRDIKPSNILLGDDGHVXIADFCVSNOF 300 Qy 301 EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360 Bb 301 EGNDAQLSSTAGTPAFWAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDFILA 360 Qy 361 LHRKIKNEPVYFPEEPEISBELKDLILKMLDKNPETRIGVPDIKLHPWYTKNGEEPLPSE 420 A1 LHRKIKNPAVFPEEPEVSEELKDLILKMLDKNPETRIGVPDIKLHPWYTKNGEEPLPSE 420 Qy 421 EEHCSVVEVTEGEVKNSYRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL 480 Bb 421 EEHCSVVEVTEGEVKNSYRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL 480 Qy 481 LVKEGFGEGGKSPELPGYQEDEAAS 505 481 LVKEGGGGGGKSPELPGYQEDEAAS 505	RESULT 2 JCS669 Ca2+/calmodulin-dependent protein kinase kinase (BC 2.7.1) beta chain - rat C;Species: Ratuus norvegicus (Norway rat) C;Species: Ratuus norvegicus (Norway rat) C;Bate: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 24-Sep-1999 C;Accession: UC5669; PC4493 R;Kitani, T; Okuno, S; Fulisawa, H. A;Title: Molecular cloning of Ca2+/calmodulin-dependent protein kinase kinase beta A;Reference number: JC5669; MUID:97420710; PMID:9276695 A;Accession: UC5669; MUID:97420710; PMID:977695 A;Accession: UC4493 A;Accession: PC4493 A;Accession: PC4493 A;Accession: PC4493 A;Accession: PC445) A;Accession: PC445) A;Accession: C;Cyuperfamily: unaseigned Ser/Thr or Tyr-specific protein kinase C;Superfamily: unase homology kIN> F;162-445/Domain: ATP-binding #status predicted <cab> F;162-445/Domain: ATP-binding #status predicted <cab> F;162-445/Domain: ATP-binding #status predicted <cab></cab></cab></cab>	Query Match 56.7%; Score 1494; DB 2; Length 587; Best Local Similarity 64.5%; Pred. No. 4.7e-59; Arches 283; Conservative 75; Mismatches 55; Indels 26; Gaps 3; QY 64 ARPSLSARKLSLGERPAGSYLEAQAGPYATGPASHISPRAWR 105

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A,Accession: S2632
A,Molecule type: DNA
A,Gossion: S26432
A,Molecule type: DNA
A,Cossion: 1-1142
B,Hovland, P.G.; Sclafani, R.A.
Submitted to the EMBL Data Library, August 1994
A,Description: PAKI: DNA Polymerase Alpha Suppressing Protein Kinase.
A,Accession: 847952
A,Accession: 847952
A,Accession: S47952
A,Reference number: S47952
A,Reference number: BMBL:U13398; NID:G53279; PIDN:AAC49840.1; PID:G532798
B,Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, Submitted to the EMBL Data Library, February 1993
A,Accession: S43223
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C.Species: Saccharomyces cerevisiae)
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Date: 28-Jan-1995 #sequence revision 12-May-1995 #text_change 23-Mar-2001
C.Accession: S50632; S47952; S43223
R.Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                              IAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCDKP-FSEEQARLYLRD
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                           Gaps
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submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9781, 8198,
A;Reference number: S50437
                           Indels
                                                                    SVIPGSTSRLLPARPSLSARKLSLQER--PAGSYLEAQAGPYATG-
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A;Cross-references: SGD:S0000931; MIPS:YER129w
                           67;
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C;Genetics:
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A; Accession: $58666
A; A; Accession: $58666
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-652 < MAT>
A; Residues: 1-652 < MAT>
A; Cross-references: GB:D45882; NID:g1041184; PIDN:BAA08301.1; PID:d1008896; PID:g1041185
B; Purnelle, B.; Goffeau, A.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
                                                                                                         A,Cross-references: EMBL:AB016838, NID:g6624198; PIDN:BAA77824.3; PID:g6624199
A;Experimental source: strain Bristol N2
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc C;Keywords: ATP; brain; calmodulin binding; phosphotransferase; protein kinase F;19-302/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 3
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
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A;Experimental source: strain 972h-; cosmid c297
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                                                                                                                                                                                                                                                                                                                                                                                                                          SQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGFV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFEGNDAQLSSTAGTPAFWAPEAISDSGQSF-SGKALDVWATGVTLYCFVYGKCPFIDDF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPL 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: SchizoBaccharomyces pombe
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 10-Dec-1999
C;Accession: S58666; T41270
EMBC 914, 3325-3338, 1995
A;Title: A novel protein kinase gene sspi(+) is required for alteration of g
                                                                                                                                                                                                                                                                                                                                                            SESYIQINQYRLMEEIGGGSYGIVKLAYNEEDKNLYALKVLDKMKLLKNFACFRQPPFRR
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                            5,
                                                                                                                                                                                                                                              Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERGENCHLVTVTEEEIENCVRVIPRLDTLILVXAMGHRKRFGNPF 356
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A;Reference number: Z21682; MUID:96210015; PMID:8631893
A;Accession: T37317
                                                                                                                                                                                                                                                                                            82;
                                                                                                                                                                                                                                              39.6%; Score 1043; DB 2; 57.2%; Pred. No. 1.9e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: Z21983
A;Accession: T41270
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-357 <EDE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: unassigned Ser/Inr or 171-5200000 C;Keywords: ATP C;Keywords: ATP P;133-409/Domain: protein kinase homology <KIN> F;141-149/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                         64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 620;
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- yeast (Sacchar
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A;Experimental source: strain S288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Note: YGL179c
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; transmemt
E;48-344/Domain: protein kinase homology «KIN»
F;56-64/Region: protein kinase ATP-binding motif
F;256-272/Domain: transmembrane #status predicted <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable serine/threonine-specific protein kinase (BC 2.7.1.-) YGL179c - yeast (Sacci Probable serine/threonine-specific protein G1618
C;Species: Saccharomyces cerevisiae
C;Date: 28-0ct-1995 #sequence revision 03-Nov-1995 #text_change 19-Apr-2002
C;Accession: S57252; S64196; S56168
R;Coglievina, M; Bertani, I; Kilma, R; Zaccaria, P; Bruschi, C.V.
Yeast 11, 77-774, 1995
A;Title: The DNA sequence of a 7941 bp fragment of the left arm of chromosome VII of ation and a putative serine/threonine protein kinase gene.
A;Reference number: S57252; MUID:95397594; PMID:7668046
A;Accession: S57252
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-560 <CCG
A;Cross-references: EMBL:X83690; NID:9794143; PIDN:CAA58659.1; PIDS:9794144
R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Kilma, R.; Zaccaria, P.; Delneri, D. submitted to the Protein Sequence Database, May 1996
A;Accession: S64183
A;Accession: S64184
A;Accession: S64184
A;Accession: S64184
A;Accession: S64184
A;Accession: S64185
A;Cross-references: EMBL:Z72701; NID:91322788; PIDN:CAA96891.1; PID:e243787; PID:9133
--VLREVMIMKTLEHPNIVNLIEVIDDPEFDD 177
                                                                                                                                                                                                                                        TGVTLYCFVYGKCPFIDDFILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GV-----SNQFEGNDAQL--SSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYC 345
                                                                                          ----PGALGEITARKYLRDVVAGLMYLHAHNVIHGDIKP
                                                                                                                                                   SNLLLGDDGHVKIADFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWA
                                                                                                                                                                                                                                                                 287 VGVTLYCMILGQYPFLGDTLQDTYDKIVHNPLIIPE--GLNPRLRDLIEGLLCKDPNQRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYLVFDLL------RKGPVMEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKP
                                                                                                                                                                                232 DNLLVTSTGRVKIGDFSVS---QDDDDQLRRSPGTPVFTAPECC--LGITYSGRSADTWA
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; Pred. No. 1e-15;
58; Mismatches 115;
                                                                                                                                                                                                                                                                                                                          GVPDIKLHPWVTKNGEEPLPSE 420
                                                                                                                                                                                                                                                                                                                                                     345 TLKAVAEHPWIT--GEDGAISE 364
                      RLRVAP----SETAMGD----
                                                                                                          178 FYMVLEYVDGKWAYDDSGP
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A;Cross-references: SGD:S0003147
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R; Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, February 2000
A; Reference number: Z24467
                  C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase C;Stywords: ATP; phosphorransferase; protein kinase F;131-448/Domain: protein kinase homology <KIN; F;131-448/Domain: protein kinase homology <KIN; F;139-147/Region: protein kinase ATP-binding motif
                                                                                                                                                                           14;
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                                                                                                                                                                                                                                                                                                                                                                                           249
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                                                                                                                                                                                                                                                                                                 141 VVRLAYNESEDRHYAMKVLSK--KKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQ 198
                                                                                                                                                                                                                                                                                                                            303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNSVRLIPSWITVILVKSM-----LRKRSFGNPFEPQARREERSMSAPGNLLVKEG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serine/threonine-protein kinase-like protein - Arabidopsis thaliana
NyAlternate names: protein T14D3.180
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Pate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                              ----LNOYKLOSEIGKGAYG
                                                                                                                                                                                                                                                      86 HISSSLAKTPTTTSSFCSSGSSKNKVKETNRISLTYDPVSKRKVLNTYEIIKELGHGQHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVS-----NQFEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DA----QLSSTAGTPAFMAPE-AISDSG-----QSFSGKA----LDVWATGVTLYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVXLIEVLDDPAEDN
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 3
A;Introns: 86/3; 111/3; 126/3; 151/3; 181/1; 222/3; 251/3; 312/3; 339/1
A;Note: T14D3.180
                                                                                                                                                                     Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                            Length 1142;
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                                                                                                                          21.5%; Score 566; DB 2; L. 31.6%; Pred. No. 5.2e-18; ive 82; Mismatches 135;
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A;Aolecule type: DNA
A;Recidues: 1-382 <JOR>
A;Cross-references: EMBL:ALl38649
                                                                                                                     Ouery Match
Best Local Similarity 31.69
Matches 151, Conservative
Map position: 5R Superfamily: unassigned
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Best Local Similarity
Matches 119; Conserv
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Qy 293 DFGVS	A;Tille: Characterization of a Sorginum Dicolor gene lamily encouring purecive procession A;Reference number: Z18177; MUID:98145442; PMID:9484448 A;Accession: T14736 A;Actube: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-440 cANN> A;Cross-references: EMBL:Y12465; NID:g2632253; PIDN:CAA73068.1; PID:g2632254 A;Experimental source: cultivar TX 430 C;Genetics: A;Gene: SNFL2 A;Gene: SNFL2 A;Gene: SNFL2 A;Gene: SNFL2	C; Superfamily: unassigned Ser/Inf of Tyr's specific protein Kinase nomono C; Superfamily: unassigned Ser/Inf of Tyr's specific protein Kinase C; Keywords: phosphotransferase; serine/threonine-specific protein Kinase Query Match Best Local Similarity 29:5%; Pred. No. 3.3e-13; Indels 70; Gaps 11; Matches 119; Conservative 75; Mismatches 139; Indels 70; Gaps 11; QY 124 QINQYKQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPRGSQAAQ 183 ::: :	QY 184 GGPAKQLIPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPC 243	361 LHRKIRNEPUVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWYTKNGEEP
Db 209 GVAMSTATGSTNIQSSHEQLLKSRAGTPAFFAPELCSTEKEYSCSSAIDIWSLGVTIYC 268 Qy 346 FVYGKCPFIDDFILALHRKIKNEPVYPFEEPEISEELKUDLIKMLDRN 393 269 LIFGKLPFNANSGLELPDSTIARLHRKIKNEPVYPFEEPEISE	A;Cross-references: EMBL:Ali30002; GSPDB:GN00116; NGSP:BZA19.190 A;Experimental source: BAC clone B2A19; strain OR74A C;Genetics: A;Gene: NGSP:BZA19.190 A;Map position: 6 A;Introns: 95/2 A;Introns: 95/2 Guery Match Best Local Similarity 21.5%; Pred. No. 1.1e-13; Matches 165; Conservative 91; Mismatches 168; Indels 344; Gaps 21;	QY 37 PTRNGVDPPPRARAASVIPGSTSRLLPARPSLSARKLSLQERPAGSYLE 85		Db 289 ARSLGRDSSIPSFAGDWLGLSSRVTSRAPSRTQSMKSISRSNTPQPSEPDHASIASVVPE 348 Qy 232

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A;Cross-references: GB:D26602; NID:g496384; PIDN:BAA05649.1; PID:g496385 C;Function:
G;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonic;Superfamily: AMP-activated protein kinase; protein kinase homology C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase for protein kinase homology «KIN»
F;17-271/Domain: protein kinase ATP-binding motif; F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable serine/threonine protein kinase (EC 2.7.1.-) SNFL3 - sorghum
NiAlternate names: SNF1 protein kinase homolog SNFL3
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C;Accession: T1482
R;Annen, F.; Stockhaus, J.
Bot. Acta 111, 137-142, 1998
A;Fitle: SNFL3 a protein kinase homolog of Sorghum bicolor with a high similarity to the A;Fitle: SNFL3 a protein kinase homolog of Sorghum bicolor with a high similarity to the A;Accession: T1482
A;Accession: T1482
A;Accession: T1482
A;Accession: L461 cANN>
A;Residues: 1-461 cANN>
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C;Keywords: phosphotransferase; protein kinase
F;10-266/Domain: protein kinase homology <KIN>
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                                                                                                                                                                                                                                                                                                                                                                           125 LNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 DAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHR 363
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A;Experimental source: cultivar TX 430
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                           16 LRNYKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKI
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                                                                                                                                                                                                                                                                      16.6%; Score 436.5; DB 1
33.7%; Pred. No. 1.2e-12;
iive 64; Mismatches 94
                                                                                                                                                                                                                                                                                               1 Similarity 33.77
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Best Local S:
Matches 96
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Best Local S
Matches 111
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                                                                                                                            probable serine/threonine kinase (EC 2.7.1.-) SNF11 - sorghum
N.Alternate names: SNF1 protein kinase homolog SNF11
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
R;Annen, F., Stockhaus, J.
Plant Wol. Biol. 36, 529-539, 1998
A;Title: Gharacterization of a Sorghum bicolor gene family encoding putative protein kin A;Reference number: Z18177; MUID:98145442; PMID:9484448
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Serine-threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jun-2000
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jun-2000
S;Muranaka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 NHGRMREDEARRYFQQLINAVDYCHSRGVYHRDLKPENILLDSYGNLKVSDFGLSALSQQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 GGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME-VP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNILLIGDDGHVKIADFGVS--NQF 300
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A, Cross-references: EMBL: Y12464; NID: 92632251; PIDN: CAA73067.1; PID: 92632252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 LHRKIKNEPVVFPEEPRISELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEP----
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protei
C;Keywords: phosphotransferase; serine/threonine-specific protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.6%; Score 437; DB 2; Length 440; 29.7%; Pred. No. 1e-12; ive 72; Mismatches 136; Indels
DSEQEFKRETRFTSKCPPKEIVRKIEEAAKPLGFGVQKKNYKL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tase of Saccharomyces cerevisiae.

A;Reference number: A56009; MUID:94217693; PMID:8164654
A;Accession: A56009
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A;Molecule type: DNA
A;Residues: 1-440 <ANN>
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Best Local Similarity 29.74
Matches 114; Conservative
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A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
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R;LeGuen, L.; Thomas, M.
Gene 120, 249-254, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jun-1999
C;Accession: JC1446; S58266; S66334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                    273 NSAKIKHDTTRDKVCNGEATTSNSIE-CSNSEETRGSSS-----LPNLNAFDII-SLSTG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAQLSSTAGTPAFWAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- 411
                                                                                                                                                                        ------NGEEPLPSEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRK 456
                                                        214
                    NQFEG--NDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFID 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                probable serine/threonine-specific protein kinase (EC 2.7.1.-) SNF1 - potato N;Alternate names: StubSNF1 protein C;Species: Solanum tuberosum (potato) C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jan-2000 C;Accession: T07788 Filakartos, L. Banfallyi, Z. submitted to the BNBL Data Library, January 1997 A;Reference number: Z16133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-512 <LAK×
A;Cross-references: BMBL:U83797; NID:g1935915; PIDN:AAB52224.1; PID:g1935916
C;Genetics:
                                      GPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 INOYKLOSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQG
                                                                                               DFILALHRKIKNEPVVFPEEPRISEELKDLILKMLDKNPETRIGVPDIKLHPWVTK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 KIKGGYITLPS--HLSAGARDLIPRMLIVDPWKRMTIPBIRLHPW 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 KIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPW 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T07788
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                       457 RSFGNPFEPQ-ARREER 472
                                                                                                                                                                                                                                                                                         FDLSNLFEEKYGRREER 342
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Matches 96; Conserv
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C; Function:
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A; Accession: JC1446
A; Molecule type: DNA
A; Residues: 1-212 cLb3A
A; Reference sees GB: M93023; NID: g166599; PIDN: AAA32736.1; PID: g166600
B; Trichner, M; Teuber, M; Teuber, R; Dittrich, P.
B; Thus mulber: S58256
A; Accession: S58266
A; Accession: S58266
A; Accession: S58266
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 144-198 cThU>
A; Residues: 144-198 cThU>
A; Residues: Liferential accumulation of the transcripts of 22 novel protein kinase genes i: A; Teuber, B; S51-565, 1995
A; Teuber, B; Teuber, B; S51-565, 1995
A; Teuber, B; Teuber, B; S51-565, 1995
A; Teuber, B; Teuber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein A;Reference number: JC1446; MUID:93013041; PMID:1339373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K-PFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQFEGN 303
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Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.2%; Score 426.5; DB 1;
34.0%; Pred. No. 3.3e-12;
tive 59; Mismatches 98;
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Best Local Similarity 34.0°
Matches 97, Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 12, 2004, 01:20:58 ; Search time 53 Seconds (without alignments) 496.140 Million cell updates/sec Run on:

US-10-690-617-2 2634 1 MEGGPAVCCQDPRAELVERV......FGEGGKSPELPGVQEDEAAS 505 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters:

141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P50526 schizosacch						mus musc	xenobns	Q00372 candida gla			Q12263 saccharomyc		homo sar	4			homo sa		Q09137 rattus norv	rattu	homo	homo	homo	drose	_	P15791 rattus norv	P25389 saccharomyc	homo	096017 homo sapien	•	831 homo	5512 mus musculu
Des	P50	P38	P43	P52	460	980	<u>0</u> 90	091	000	P06	074	012	800	015	091	P2532	P34	013	091	600	P11	P54	090	Q8t	061	Z6O	P15	P25	160	960	P11	015	002
ID	SSP1 SCHPO	PAK1 YEAST	KGS9_YEAST	SNF1 CANAL		KI10 ARATH	DCK1 MOUSE	STEL XENLA	SNF1 CANGA		SNF1 SCHPO	GIN4 YEAST	DCK1_RAT	DCK1_HUMAN	STKB XENLA	KMLC DICDI	KAPC_DICDI	KCCG HUMAN	STK6 XENLA	AAK2 RAT	KCCG RAT	AAK2 HUMAN	ARK5 HUMAN	KIII HUMAN	LOK DROME	KCCG MOUSE	KCCD RAT	KCC4 YEAST	KCCA HUMAN	CHK2 HUMAN	KCCA RAT	STKB HUMAN	MRK2_MOUSE
DB		_	-		급		_	-	H	_	_	H		н	-	-	~	-	Н	н	-1	,-1	-	-	-		Н	н		-	,	-	7
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Query	23.5	H	19.3	16.6	16.4	16.2	15.7	15.6	15.5	15.3	15.3	15.3	15.3	15.2	15.1	15.0	15.0	7	14.8	14.8	14.8	14.	14	14.7	14.7		14.6	4	14.6	14.6	14.6	14.5	14.5
Score	620	566	507.5	437	432	426.5	412.5	410	407	403.5	403	403	402.5		397	396	394	393	390.5	389.5	389	387.5	387	387	386	385.5	384.5	84	384	8		383	æ
Result No.		8	m	4	Ŋ	v	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P11798 mus musculu	Q13557 homo sapien	Q09170 schizosacch	Q13554 homo sapien	P21137 caenorhabdi	P28652 mus musculu	P05132 mus musculu	P31751 homo sapien	P17612 homo sapien	Q13131 homo sapien	O42626 neurospora	P22987 schizosacch	
KCCA MOUSE	KCCD_HUMAN	CDS1_SCHPO	KCCB HUMAN	KAPC CAEEL	KCCB MOUSE	KAPA MOUSE	AKT2 HUMAN	KAPA HUMAN	AAK1 HUMAN	NRC2 NEUCR	KIN1_SCHPO	
Н	Н	Н	Н	н	ч	1	ч	Н	П	Н	н	
478	499	460	664	404	542	350	481	350	550	623	891	
14.5	14.5	14.5	14.4	14.4	14.4	14.3	14.3	14.3	14.3	14.3	14.3	
382.5	382.5	382	378.5	378	378	377	377	375.5	375.5	375.5	375.5	
34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT SSP1_S ID_Si	SSPI SCHPO ID SSPI SCHPO	STANDARD;	OARD	-	PRT;	652	AA.
N L		(Rel. 3	Ω,	Created)		1	ĵ
i d d	01-OCT-1996 28-FEB-2003	(Rel. 34, Last 8 (Rel. 41, Last 8	, '.	ast st ast an	sequence update; annotation update)	upaat n upd	ce/ date)
DE	Serine/threonine-protein kinase ssp1 (EC 2.7.1) ssp1 OR SPCC347.03.	nine-pro	otei	n kina	se sspl	(EC	2.7.1).
So	Schizosaccharomyces pombe (Fission yeast)	romyces	mod	be (Fi	ssion y	east)	
88	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	ungi; A	BCOM	ycota;	Schizo	Bacch	naromycetes;
38	SchizoBaccharomycetales; SchizoBaccharomycetaceae; SchizoBaccharomyces.	romyces	р П	3	בייסמכרניי	7	Y ceraceae,
X	NCBI TaxID=4896;	1968					
R R	SEOUENCE FROM N.A	M N.A.					
RC	STRAIN=972;						
۲ ۲	MEDLINE=9535	4651; P	ubMe	d=7628	1434;	É	MBDLINE=95354651; PubMed=7628434;
\$ £	"A novel pro	, Hirati Fein kin	a D.	, rank	gida m. sspl+ i	s, rec	da 1.; quired for alteration of
RI	growth polar	ity and	act	in loc	alizati	i no	growth polarity and actin localization in fission yeast.";
RL	EMBO J. 14:3	325-333	8 (19	. (36)			
RN	[2]	:					
RP	SEQUENCE FROM N.A.	A.N.					
2 K	STRAIN=9/2; MEDI.INE=21848401: PubMed=11859360;	8401 · P	AM4.	d=1186	9360;		
Z A	Wood V. Gwi	lliam R	2	ajandı	ream M.A	3	yne M., Lyne R., Stewart A.,
æ	Sgouros J.,	Peat N.	Ha	yles .	I., Bake	S.	, Basham D., Bowman S.,
RA	Brooks K., B	rown D.	, Br	S TWO	Chill	ingw	orth T., Churcher C.M.,
RA I	Collins M.,	Connor	.; ≃;	Croni	A., Da	917	P., Feltwell T., Fraser A.,
¥ 6	Gentles S.,	Goble A	. F	HOWAL	Th S	Hick	D., Aldalyo U., Hougson G., le E.J., Hunt S., Jagels K.,
§ §	James K., Jo	nother,	. O.	les M.	Leathe	S	, McDonald S., McLean J.,
Z.	Mooney P., M	foule S.	Σ.	ingall	K., Mur	phy 1	A Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
8 8	Oliver K., C	Neil S	 	earson	o, Oct	ומזן ן כי	M.A., Rabbinowitson E.,
5 8	Skelton J.	Simmond	S K	Squi	ares R.,	Squ	ares S., Stevens K.,
Z.	Taylor K., T	aylor R	Ö	Tive	/ A., Wa	lsh :	S.V., Warren T., Whitehead S.,
R3	Woodward J.,	Volcka	ert	., A	ert R.,	Robb	en J., Grymonprez B.,
A G	Gabel C Fu	rhs M	מנה היד	LZC C	Holze	, H	. Moestl D., Hilbert H.,
§ §	Borzym K., I	anger I		seck A	, Lehra	ch H	., Reinhardt R., Pohl T.M.,
RA	Eger P., Zin	mermann	3	Wedl	er H., W	ambu	tt R., Purnelle B.,
RA	Goffeau A.,	Cadieu	, M	Drean	S., G.	S t	S., Lelaure V., Mottler S.,
8 6 8	Galibert F.,	Aves S	. ₍	Xiank	J Z., HU	nr Talla	., Moore A., Huist S.M., ada V.A Garzon A., Thode G.,
5 S	Daga R.R., C	ruzado	, i	Jimen	3 J., S	anch	ez M., del Rey F., Benito J.,
RA	Dominguez A.	, Revue	1ta	J.L.,	Moreno	S., .	Armstrong J., Forsburg S.L.,
R.A	Cerrutti L.,	Lowe T	<u>.</u>	4cComb	ie W.R.,	Pau	Cerrutti I., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
3 1	Shpakovski	3.V., UB	ser,	D.,	3arrell	9 . e	Nurse F.;
X 1	"Ine genome sequence or Nature 415.871-880(2002)	sequenc	2002	ocur.	COBACCITO	r Cilling	ces pompe.
2 2 2 3	-!- FUNCTION	I: Invol	ved	in ac	in loca	liza	-!- FUNCTION: Involved in actin localization and thus in polarized

-!- FUNCTION: Involved in actin localization and thus in polarized cell growth.
 -!- SUBCELLUIAR LOCATION: Cytoplasmic (Probable).
 -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

PRT; 1142 AA

STANDARD;

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YEAST
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 VEPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEP----LPSEERHCSV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 VEVTEGEVKNSVRLIPSWITVILVKSMLRKRSFGNPF---EPQARREERSMSAPGNLLVK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEVPPSVFPEYPVHKAIQKTSDSFRKRNYSAGDYVIAPLGGEREGSSLTHSWTFQPGKHN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 GKVKLGRDTVTRELLAIKIIPKTE------RPP-----KLGRANASSQKEKVRRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78;
                                                                                                                                         EMBL; D45882; BAA08301.1; -.

REMBL; AL049609; CAB40783.1; -.

RIP; S58666; S58666.

R GeneDB SPombe; SPCC297.03; -.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR002290; Ser_thr_pkin AS.

R InterPro; IPR002290; Ser_thr_pkin AS.

R Pfani; PF000609; prot kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00110; PROTEIN KINASE DOM; 1.

R PROSITE; PS00111; PROTEIN KINASE DOM; 1.

R PROSITE; PS00111; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.5%; Score 620; DB 1; Length 652; 34.4%; Pred. No. 4.5e-33; ive 67; Mismatches 176; Indels '
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B1931E5EB75A85DA CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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267 2
652 AA;
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Best Local Similarity
Matches 168; Conserv
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RESULT 2 PAK1_YEAST

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                                                                                                                                                                                                                                                                                                                                                                                          MEDIANE-2731264; PubMed-9169868;
MEDIANE-97313264; PubMed-9169868;
Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E., Araujo R., Aviles E., Berennan T., Carpenter J., Chen E., Chary J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H. Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Smith V., Taylor P., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Gen. Genet. 256.45-53(1997).
-!- FUNCTION: May function by modifying and partially stabilizing thermolabile DNA polymerases, perhaps during DNA repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- PTM: Autophosphorylated.
                                                                                                                                                                                                                                            Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hovland P.G., Tecklenberg M., Sclafani R.A.;
"Overexpression of the protein kinase Pakl suppresses yeast DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U18916; AAC03227.1; -.

EMBL; U18916; AAC49840.1; ALT_TERM.

PIR; S50632; S50632.

GermConline; 139208; -.

SGD; S0000931; PALT.

SGO; GO:0004672; F:protein kinase activity; IDA.

RGO; GO:0006468; P:protein minio acid phosphorylation; IDA.

RICETPRO; IPR009219; Prot kinase.

R InterPro; IPR008271; Ser_thr_pkin_AS.

R InterPro; IPR008271; Ser_thr_pkin_AS.
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ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS001019; PROTEIN KINASE ST; 1.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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ATP (BY SIMILARITY).
BY SIMILARITY.
Q -> H (IN REF. 2).
EYL -> DS (IN REF. 2).
ATP (BY SIMILARITY).
                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Serinc-threonine-protein kinase PAKI (EC 2.7.1.-)
PAKI OR YER129W OR SYGP-ORF45.
                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98000885; PubMed=9341678;
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Mol. Gen. Genet. 256.4
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STRAIN=S288c / AB972;
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266 26
1142 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 DA----QLSSTAGTPAFMAPE-AISDSG-----QSFSGKA----LDVWATGVTLYC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- BELKDLILKMLDK 392
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                                                                                                                                                                                                                  141 VVRLAYNESEDRHYAMKVLSK--KKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQ 198
                                                                                                                                                                                                                                                EIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCD------KPFSE 249
                                                                                                                                                                                                                                                                                                                                                                                   192 EIAIMKKCHHKHVVQLIEVLDDLKSRKIYLVLEYCSRGEVKWCPPDCMESDAKGPSLLSF 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 EQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVS-----NQFEGN 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNSVRLIPSWTTVILVKSM-----LRKRSFGNPFEPQARREERSMSAPGNLLVKEG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||:| : ::||: | |::| || KNAVSGVGKKIKESVLKSIPLKDPSDLSNKNYLHPTETTRGRGD-----ANVIVSEG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95397594; PubMed=7668046; Coglievina M., Bertani I., Klima R., Zaccaria P., Bruschi C.V.; Coglievina M., Bertani I., Klima R., Zaccaria P., Bruschi C.V.; "The DNA sequence of a 7941 bp fragment of the left arm of chromosome VI of Saccharomyces cerevisiae contains four open reading frames including the multicopy suppressor gene of the pop2 mutation and a putative serine/threonine protein kinase gene.";
                                                                                                     HISPRAWRRPTIESHHVAISDAEDCVQ------LNQYKLQSEIGKGAYG
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-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
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Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                 Pred. No. 3e-29;
; Mismatches 135; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable serine/threonine-protein kinase YGL179C (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 FVYGKCPFIDDFILALHRKIKNEPVVFPEEPEIS-----
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EMBL; X83690; CAA58659.1; -.
EMBL; Z72701; CAA96891.1; -.
PIR; S57252; S57252.
HSSP; Q00534; IBI8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288c / FY1679;
                    Similarity
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P43637;
                                                  151;
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                    Local
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329 PDKRIKLADIKVHPFMCHYGKSDAASVLTNLETFHELKVSPPSSCKRVELVSLPVNSSFA 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 INQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKOYGFPRRPPPRGSQAAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --MEVPCDKP--FSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 PETRIGVPDIXLHPWVTKNGEEPLPS-----EEEH------CSVVEVTEGEVKNSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 GPAKQL-LPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 LLFGKLPFNANSGLELFDSIINKPLEFPSYEEMINGATSGITMEEYTDAKDLLKKLLQKD
SGD; S000147; TOS3.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Prot thr pkin AS.
InterPro; IPR000220; Ser thr pkin AS.
Pfam; PF00069; pkinase; 1.
Probom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS0011; PROTEIN KINASE ST; 1.
Hypothetical protein; Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 32354 / B-311;
MEDLINE=98053924; PubMed=9393775;
MEDLINE=98053924; PubMed=9393775;
Petter R., Chang Y.C., Kwon-Chung K.J.;
"A gene homologous to Saccharomyces cerevisiae SNF1 appears to be essential for the viablilty of Candida albicans.";
Infect. Immun. 65:4909-4917(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 560;
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EFFA0CSED58B5466 CRC64;
                                                                                                                                                                                                                                                                                                                                                    19.3%; Score 507.5; DB 1; 35.2%; Pred. No. 7.8e-26; tive 58; Mismatches 115;
                                                                                                                                                                                                                                                       ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
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                                                                                                                                                                                                                                      PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                 62090 MW;
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                                                                                                                                                                                                                                                                                                                                                                                          Matches 128; Conservative
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64
79
189
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56
79
189
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                                                                                                                                                                                                                      ATP-binding.
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SEQUENCE
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NP BIND
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EMBL; AB024535; BAA75889.1; -.
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                                                                                                  469 REERSMSAPGNLLVKEG-
                                                                                                                                                                                                                                                                                                                                                               Candida tropicalis (Yeast)
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81
174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subfamily.
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                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 QLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 GGPAKQLLPLERVYQEIAILKKLDHVNVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPC 243
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                                                                                                                                                                                         -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 DKPFSEEQARLYLRDVILGLEYLHCOKIVHRDIKPSNLLLGDDGHVKIADFGVSN-QFEG
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ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
                                 STRAIN-ARCC 32354 / B-311;
Petter R., Kwon-Chung K.J.;
Submitted (MAR-1986) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Essential for release from glucose repression. It interacts and has functional relationship to the regulatory protein SNF4. Could phosphorylates CAT8 (By similarity).
-!- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQ -> AR (IN REF, 2),
AGPEVDV -> SSVQKLMI (IN REF, 2).
YVMLCGRLPFDDEF -> GMSCCVVDXHSWTSS (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.6%; Score 437; DB 1; Length 620; 29.1%; Pred. No. 3.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 3.5e-21;
78; Mismatches 137; Indels
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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A -> R (IN REF. 2).
R -> A (IN REF. 2).
S -> L (IN REF. 2).
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HSSP; Q63450; 1A06.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR002290; Ser_thr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L78129; AAB48643.1; -.
[2]
SEQUENCE OF 7-620 FROM N.A.
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les 122; Conserv
                                                                                                                                                                         similarity).
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CONFLICT
CONFLICT
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NP BIND
BINDING
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                                               VTKNGEEPLPSEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQAR 468
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                                                                                                                                                                                                                            371 SSNEILDA--YLLMKENHALVKDLKKSKSENIESFLSQSPPPSPFPNRGSTSSAPGVQQ 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tropicalis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kanai T., Ogawa K., Ueda M., Tanaka A.;
"Genetic evaluation of the function of SNF1 in Candida tropicalis."
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Essential for release from glucose repression. It interacts and has functional relationship to the regulatory protein SNF4. Could phosphorylates CATB (By similarity).
-!- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; pkinase; I. SMCDOM; PD000001; Prot kinase; I. SMART; SM00220; STKr; I. PROSITE; PS00107; PROTEIN KINASE ATP; I. PROSITE; PS00108; PROTEIN KINASE ST; I. PROSITE; PS50011; PROTEIN KINASE DOM; I. Transferase; Serine (threonine-protein kinase; ATP-binding; Phosphorylation; Carbohydrate metabolism; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (AUTO-) () 00 OFCF1FC3DCE706D7 CRC64;
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InterPro; IPR008271; Ser Thr pkin AS.
InterPro; IPR002290; Ser thr pkinase.
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Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Salanoubat M., Lemcke K., Rieger M., Parer-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
De Simone V., Choisne N., Ariguenave F., Robert C., Brottier P.,
Nancker P., Cattolico L., Weisenbach J., Saurin W., Quetier F.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Nurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
Nurmbach E., Drzonek H., Voss H., Holland R., Brandt P., Nyakatura G.,
R. Wezdl A., D'Angelo M., Pallavicini A., Toppo S., Simionari B.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Reichelt J., Scharfe M., Berger-Liaurc C., Purnelle B., Masuy D.,
de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
Monfort A., Argiritou A., Flores M., Liguori R., Vitale D.,
Monfort A., Argiritou A., Flores M., Liguori R., Vitale D.,
Monfort A., Argiritou A., Flores M., Liguori R., Vitale D.,
Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
                                                                                                                                  202
                          303 NDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALH 362
                                                                                                                                                                                                         --PDIKLHPWV 409
                                                                                                                                                                                                                                                                                                                    259 KKISNGVYILPN--YLSPGAKHLLTRMLVVNPLNRITIHEIMEDEWFKQDMPDYLLPPDL 316
                                                                                                                                                                                                                                                                                                                                                                 410 TKNGEEPLPSEEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARR 469
                                                                                       244 DKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSN-QFEG 302
                                                                                                                                                                                                                                                                                                                                                                                             SKIKTSKIDIDEDVISALSVIMGYDRDEI-----ISVIEKANREAAAGGA-TPINQS 367
GGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GFGEGGKSPELPGVQE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 KSTNEVLDAYLLMKENHTLVKDLKKSKSENIESFLSLSPPPSSSFPNPGSTSSAPGVQQ 426
                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=930113041; PubMed=1339373; le Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.; le Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.; Structure and expression of a gene from Arabidopsis thaliana encoding a protein related to SNF1 protein kinase."; Gene 120:249-254(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
Lessard P., Kreis M., Thomas M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIIO ARATH STANDARD; PRT; 535 AA.
038997; O04728; Q39076; Q8RWD2;
15-JUL-1999 (Rel. 38, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
SNF1-related protein kinase KIN10 (EC 2.7.1.-) (AKIN10)
KIN10 OR SKIN10 OR AT3601090 OR T4P13.22.
                                                                                                                                                                                                                                                                         363 RKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGV--
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MEDLINE=21016720; PubMed=11130713;
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE Columbia;

MEDLINE=22594860; PubMed=14593172;

MEDLINE=22594860; PubMed=14593172;

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldenth A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

Satou M., Tamse R., Vayaberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
Creaby T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militscher J., Sellers P., Gill J.B., Feldblyum T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Fraser C.M., Kaneko T., Namura Y., Sato S., Kato T., Asamizu E., Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Mateumoto M., Matsuno A., Muraki A., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=038997-2; Sequence=VSP 009001;
TISSUB SPECIFICITY: Expressed in roots, shoots and leaves.
SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOI, Gen. Genet. 245:390-396(1994).
-!- FUNCTION: May play an important role in a signal transduction
cascade regulating gene expression and carbohydrate metabolism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      le Guen L., Thomas M., Kreis M.; "Gene density and organization in a small region of the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sold=Q38997-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 UBA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Columbia;
MEDLINE=95115691; PubMed=7816049;
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EMBL; BT01038, AA056829.1; -.
EMBL; X94757; CA64384.1; -.
PIR; JC1446; JC1446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M93023; AAA32736.1; -.
EMBL; X79707; CAA56146.1; -.
EMBL; AC008261; AAF26165.1; -
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InterPro; IPR001772; Kinase
InterPro; IPR000719; Prot_Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 302:842-846(2003).
                                                                                                                                                                                                                                Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        higher plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thaliana genome.";
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                                                                                                                                                                                                            thaliana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :: || | :: |: |: TKVCSSMDENDGP---GEGDELGRRHSLQRGWRR-------EESEEGFQIPATITER 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 RPAGSYLEAQAGPYATGPAS----HISPRAMRRPTIESHHVAISDAEDCVQL----NQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   499 YTERDASGMLYNLASAIXYLHSLNIVHRDIKPENLLVYEHQDGSKSLXLGDFGLATIVDG 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 LHRKIKNEPVVFPEE--PEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAQGGPA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 KQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMB-VPCDKP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 NDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPF--IDDFILA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PLYTVCGTPTYVAPEIIAETGY---GLKVDIWAAGVITYILLCGFPPFRGSGDDQEV 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     613 LFDQILMGQVDFPSPYWDNVSDSAKELINMMLLVNVDQRFSAVQVLEHPWVNDDG---LP 669
      SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING MEAN. WAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS SYSTEM (By similarity). SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CamK
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-----HMIQNEVSILRRVXHPNIVLLIEEMDVPTE--LYLVWELVKGGDLFDAITSTSK
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SMART; SM00220; S TKc; 1.
PROSITE; PS50309; DC; 2.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97;
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3DIDBF18C23129F2 CRC64;
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DOUBLECORTIN 2.
SER/PRO-RICH.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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; Pred. No. 1.8e-19;
71; Mismatches 199;
                                                                 subfamily.
SIMILARITY: Contains 2 doublecortin domains.
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MGD; MGI:1330861; Dcamkil.
InterPro; IPR00353; Dc.
R InterPro; IPR00371; Src thr pkin AS.
R InterPro; IPR008271; Ser thr pkin AS.
DR Pfam; PF03607; DCX; S.
Pfam; PF00069; pkinase; l.
ProDom; PD00001; Prot kinase; l.
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269
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298
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ACT SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KNWEMEBEKVRREIKILRLFMHPHIIRLYEVIETPTD--IYLVMEYVNSGELFDYIVE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 INQYKLOSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPAKOLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVPCD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 K-PFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQFEGN 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 194 HF-LKTSCGSPNYAAPEVI--SGKLYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFK 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78
                                                                                                                                                                                                                                                                          BY SIMILARITY.

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

Missing (in isoform 2).

/FIId=VSP_009001.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine-threonine-protein kinase DCAMKLI (EC 2.7.1.-) (Doublecortin-like and CAM kinase-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development.";
J. Neurosci. Res. 58:567-575(1999).
-!- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20004649; PubMed=10533048;
Burgess H.A., Martinez S., Reiner O.;
"KIAA0369, doublecortin-like kinase, is expressed during brain
InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR00449; UBA_domain.

Pfam; PF02149; KA1; 1.

R Pfam; PF00169; pkinase; 1.

R Pfam; PF00109; TYRKINASE.

R SMART; SM00109; TYRKINASE.

R SMART; SM00165; UBA; 1.

R SMART; SM00165; UBA; 1.

R PROSITE; PS00101; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE_ST; 1.

R PROSITE; PS0030; UBA; 1.

R PROSITE; PS0030; UBA; 1.

R PROSITE; PS0030; UBA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPW 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 426.5; DB 1; Length
Pred. No. 1.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                       98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFFC383223FD8317 CRC64;
                                                                                                                                                                                                                   Phosphorylation; Alternative splicing.

DOMAIN 42 294 PROTEIN KINASE.

NP BIND 48 56 ATP (BY SIMILARITY).

DOMAIN 315 355 UBA.
                                                                                                                                                                                                                                                                                                                                                                                                                    59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          756 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                         61181 MW;
                                                                                                                                                                                                                                                                                                                                                                                       16.2%;
34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                56
355
165
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                          535 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                315
165
71
198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCK1 MOUSE
                                                                                                                                                                                                                                                                            ACT SITE
BINDING
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DCK1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
SEEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPG 478
                                                                                                                                                                                                                                                                                                                                                                                                           Roghi C., be Guellec R., Paris J., Couturier A., Philippe M.,
"Eg2, selected by differential screening encodes a new Xenopus protein
kinase family.",
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis especially from prophase through anaphase. Partially colocalised with gamma, tubulin in the centrosome, from S to M phase (By
                        570 ENEHQLSVA----GKIKKHFNTGPKPSSTAAGVSVIATTALDK--ERQVFRRRNQD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell cycle; Transferase; Serine/Threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)

By FEB-2003 (Rel. 41, Last annotation update)

Serine(threomine protein kinase Eg2-like (EC 2.7.1.37) (p46XlEg22).

Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: Phosphorylated (By similarity). SIMILARITY: Belongs to the Ser/Thr family of protein kinases. Aurora subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%; Score 410; DB 1; Length 408; 29.9%; Pred. No. 1.2e-19; ive 61; Mismatches 155; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 BY SIMILARITY.
46461 MW; 97F6A69C7357AEE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                                                                                                                408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00107; PROTEIN KINASE ATP; 1. PROSITE; PS50011; PROTEIN KINASE DOM; 1. PROSITE; PS00108; PROTEIN KINASE ST; 1.
                                                                                                ---VRSRYKAQPAPPELNSESEDYSPS 744
                                                               479 NLLVKEGFGEGGKSPELPGVQEDEAAS 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z17206; CAA78914.1; ALT_INIT.
HSSP; P24941; 1AQ1.
InterPro; IPR000713; Prot kinase.
InterPro; IPR000871; Ser_thr_pkin_AS.
InterPro; IPR001291; Ser_thr_pkin_as.
InterPro; IPR001295; Tyr_pkinase.
Ffam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SWART; SM00220; S TKC; 1.
                                                                                                                                                                                PRT;
                                                                                                                                                                                                               Created)
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390
154
169
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263
408 AA;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
                                                                                                                                                                                                               28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                              rissue=Egg;
                                                                                                                                                                             STGL XENLA
Q91819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT SITE
SEQUENCE
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BINDING
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                                                                                                                                            RESULT 8
STGL_XENLA
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37 PTRNGVDPPPRARAASVIPG-STSRLL-----PARPSLSARK--LSLQERPAGSYLEAQA

Conservative

Local Similarity

126;

Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PATHGHQTSKPQGPNENRNPQQTSHSSTPNMEKKGSTDQGKTLAVPKEEGKKKQ 134
                                                                                                                                                                                                                                                       181 AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVM- 239
                                                                                                                                                                                                                                                                                                                                              240 EVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                     300 FEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFIL 359
24 PKRIPVSQPPSTQVRPPVTGVSAQRILGPSNVPQRVMMQAQKPVLSNQKPTAQGLLR--- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                                                                                                                                       135 WC--LEDFEIGRPLGKGKFGNVYLARERESKFILALKVLFK--------SQ
                                                                         GPYATGPASH-----ISPRAWRRPTIESHH--------VAISDAED---
                                                                                                                                                             122 - CVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPRRSQ
                                                                                                                                                                                                                                                                                                                                                                      286 VHAPSSRRTTLCGTLDYLPPEMI -- EGRNHDEK-VDLWSLGVLCYEFLVGKPPFETDTHQ
                                                                                                                                                                                                                                                                                               176 LEKAĞVEHQL-----RREVEİQSHLRHPNILRLYGYFHDAS--RVYLILDYAPGGELFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 ALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=NCCLS84;
MEDLINE=97101049; PubMed=8945576;
Petter R., Kwon-Chung K.J.;
Fishuption of the SNR1 gene abolishes trehalose utilization in the pathogenic yeast Candida glabrata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infect. Immun. 64:5269-5273 (1996).
-!- FUNCTION: Essential for release from glucose repression. It interacts and has functional relationship to the regulatory protein SNF4. Could phosphorylates CATS (By similarity).
-!- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Candida glabrata (Yeast) (Torulopsis glabrata).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EC 2.7.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
12-UUL-1999 (Rel. 38, Last annotation update)
Carbon catabolite derepressing protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  611 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000719; Prot_kinase.
Interpro; IPR008271; Ser_thr_pkin_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L78130; AAB48642.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EE 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CANGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420
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000372;
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DOMAIN
DOMAIN
NP BIND
        Science
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      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 ISDAEDCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 PRGSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SDMQG-----RIDREISYLRILRHPHIIKLYDVI--KSKDEIIMVIEYAGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 VSN-QFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 EYLVPQDLKQQEQFNKKSGNEENVEEIDDEMVYTLSKIMGYDKDEIYEALESSEDTPAYN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 GPVMEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDFILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESIPVLFKNISNGVYTLPK--FLSPGASDLIKRMLIVNPLNRISIHEIMQDEWFKVDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |::|: || ::|
EIRNAYILIKDNKSLIKDMKQDNNVTQELDTFLSQSPPTFQQNGDGMKASEDQKKKHSGR
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
89E17812A4900CD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=86289463; PubMed=3526554;
Celenza J.L., Carlson M.;
"A yeast gene that is essential for release from glucose repression encodes a protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 3.1e-19;
80; Mismatches 135; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------TKNGEEPLPSEEEHCSVVEVTE--------
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUJ-1999 (Rel. 38, Last annotation update)
Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
SNF1 OR CAT1 OR CR1 OR PAS14 OR GLC2 OR YDR477W OR D8035.20.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                15.5%; Score 407; DB 1; Length 611; 26.2%; Pred. No. 3.1e-19;
Production, irrovazav; ser thr pkinase.
Pram; PRO0069; pkinase; 1.
SWART; SM00220; STRC; 1.
SWART; SM00220; STRC; 1.
FROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS001019; PROTEIN KINASE DOM; 1.
PROSITE; PS001019; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROMING 6 17
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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53
68
161
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Best Local Simi
Matches 119;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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REALL, A26030.

RESP, P24941, IHCL.

GERMONIAN: 1005634.

ROGOGOSSA, CINCIPLER, INC.

GO, GO:0005737; C:cytoplasm; IPI.

GO; GO:000534; C:noclaus; IPI.

GO; GO:000324; C:noclaus; IPI.

GO; GO:000324; C:vacuole (sensu Fungi); IPI.

GO; GO:000324; C:vacuole (sensu Fungi); IPI.

GO; GO:000324; C:vacuole (sensu Fungi); IPI.

GO; GO:000324; P:SNFIA/AMP-activated protein kinase activity; IDA.

GO; GO:000324; P:SNFIA/AMP-activated protein kinase activity; IDA.

GO; GO:000324; P:SNFIA/AMP-activated protein kinase activity; IDA.

GO; GO:0004679; F:SNFIA/AMP-activated protein kinase activity; IDA.

GO; GO:0004679; F:SNFIA/AMP-activated protein kinase activity; IDA.

GO; GO:0004679; F:SNFIA/AMP-activated protein; IDA.

GO; GO:0004609; P:SnFIA/AMP-activated protein kinase; ATP-binding;

REALLY: PROSITE; PSO0104; PROTEIN KINASE ATP; 1.

REALLY: PROSITE; PSO0104; PROTEIN KINASE ATP; 1.

REALLY: PROSITE; PSO0104; ROTEIN KINASE ATP; 1.

REALLY: PROSITE; PSO0104; ROTEIN KINASE ATP; 1.

REALLY: PROSITE; PSO0104; ROTEIN KINASE DOM; 1.

REALLY: PROSITE; PSO0104; ROTEIN KINASE DOM; 1.

REALLY: PROSITE; PSO0104; PROTEIN KINASE DOM; 1.
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                                                                                                                       Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
Hunicke-Smith S., Hyman R., Komg C., Lashkari D., Lew H., Lin D.,
Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
Winant A., Yelton M., Botstein D., Davis R.W.,
Submitted (Aug-1995) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinase.";
J. Biol. Chem. 269:2361-2364(1994).
-!- FUNCTION: Essential for release from glucose repression. It
interacts and has functional relationship to the regulatory
protein SNF4. Interacts also with SIP1, SIP2 and GALB3. Could
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PHOSPHORYLATION (AUTO-).
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233:1175-1180(1986)
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Best Local Similarity 28.5
Matches 121; Conservative
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177
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SEQUENCE
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WEDLINE=912.

WEDLINE=1848401; PubMed=11859360;

WEDLINE=21848401; PubMed=11859360;

A Wood V. (Gailliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ra Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Rollins M., Connor R., Cronin A., Davis P., Hidelo J., Hodgeon G., A., Gorlins M., Connor R., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., R. Monorey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., A. Monorey P., Moule S., Squares R., Seeger K., Sharp S., Rutherford K., Rutter S., Sauders D., Quail M.A., Rabbinowitsch B., R. Skelton J., Simmonds M., Squares R., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Sator R., Weltjens I., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Volckaert G., Aert R., Robben J., Grymonprez B., Metjens I., Volckaert G., Aert R., Robben J., Grymonprez B., Radbel C., Fluchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabbel C., Rober B., Metjens I., Volckaert E., Rieger M., Schaefer M., Mutller-Auer S., Galbel C., Fluchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Rabbel C., Rober B., Mockier S., Galber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Galibert F., Aves S.J., Kiang Z., Hunt C., Moore K., Hurst S.M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G. Rabber B., Borzaon A., Thode G., Dagaa R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
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SDAEDCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPP 176
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                             44 SSLADGAHIGNYQIVKTLGEGSFGKVKLAYHTTTGQKVALKIINKKVLAK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) SNF1-like protein kinase (EC 2.7.1.-).
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NCBI_TaxID=4896;
                                                                                                                                                    94 ---SDMQG-
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074536;
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SNF1 SCHPO
AC 074536,
DT 15-JUL.
DT 15-JUL.
DT 15-JUL.
DE SNF1-1;
CC SCHIZCO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 IPNLFKKVNSCVYVMDD--FLSPGAQSLIRRMIVADPMQRITIQEIRRDPWFNVNLPDYL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 RPMEEVOGSYADSRIVSKLGEAMGFSEDYIVEALRSDENNEVKEAYNLLHE-NQVIQEKS 352
                                                                                      Nature 415:871-880(2002).
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KKRMTEDEGRRFFQQIICAIEYCHRHKIVHRDLKPENLLLDDNLNVKIADFGLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 INQYKLOSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQAAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 GPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYL-----VFDLLRKGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VVEV----TEGEVKNSVRLIPSWTTVILVKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 ILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPL
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DOMAIN 34 285 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.3%; Score 403; DB 1; Length 578 30.5%; Pred. No. 5.2e-19; ive 70; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (BY SIMILARITY).
BY SIMILARITY.
E5857E8F171E7B50 CRC64;
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Pot:
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
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ATP (BY SIMILARITY)
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HSSP; Q63450; 1A06.

GeneDB Spoude; SPCCT4.03c; ...

InterPro; IPR00871; Ser thr pkin AS.

InterPro; IPR00871; Ser thr pkin as.

InterPro; IPR00871; Ser thr pkin as.

InterPro; IPR00849; UBA domain.

Pfam; PF00069; pkinase; I.

PROSTE; PS00107; PROTEIN KINASE ATP; I.

PROSTE; PS00107; PROTEIN KINASE DOM; I.

PROSTE; PS00108; PROTEIN KINASE DOM; I.

PROSTE; PS00108; PROTEIN KINASE ST; I.

PROSTE; PS00108; PROTEIN KINASE ST; I.
                                                                                                                                                                               -!- SIMILARITY: Contains 1 UBA domain.
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156 156 B
576 AA; 65996 MW;
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Matches 111; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLRK 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A., Dietrich F.S., Mulligan J., Chenry J.M., Chung E., Duncan M., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Low H., Lin D., Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Minant A., Yelton M., Botstein D., Davis R.W.; Shoff and A.Y. Yelton M., Botstein D., Davis R.W.; L. FUNCTION: May play a role in septin assembly.
-: SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIMI
                                                                                                                                                                                                                                                                                                                                                                                                            and the
                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 403; DB 1; Length 1142; Pred. No. 1.2e-18; 57; Mismatches 143; Indels 44
                                                                                                                                                                                                                                                                                                                                                                            Longtine M.S., Fares H., Pringle J.R.; "Role of the yeast Gin4p protein kinase in septin assembly relationship between septin assembly and septin function."; J. Cell Biol. 143:719-736(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EC16FF4BB49DD811 CRC64;
                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Serine/threonine-protein kinase GIN4 (EC 2.7.1.-).
GIN4 OR YDR507C OR D9719.13.
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ATP (BY SIMILARITY).
BY SIMILARITY.
                          PRT; 1142 AA.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99030835; PubMed=9813093;
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                                                                           (Rel. 35, Created)
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EMBL; U33057; AAB64949.1; -.
PIR; S59359; S59359.
                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subfamily.
                                                                           01-NOV-1997
                             GIN4 YEAST
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                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                    302 GNDAQLSSTAGTPAFMAPBAISDSGQSFSGKALDVWATGVTLYCFVYGKCPF--IDDFIL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 TLLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLQKYPSIRDSK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTK-----N 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEEPLPSEEEHCSVVEVTEGEVKNSVRLIPSWTTVIL-----VKSMLRKRSFGNPFE 464
                                  67
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Mangelus M., Silverman M.A., Kedar H., Naor C., Kornuc M., Hanoch T.,
Seger R., Theill L.E., Nedivi E., Richter-Levin G., Citri Y.;
"Hippocampal plasticity involves extensive gene induction and multiple
cellular mechanisms."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CaMK
                                                                                                                                                    ---NTGNVSGTSIVG
                                                                                                          GPAKOLLP--LERVYOEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVMEVP
                                                                                                                                                                                                                                                           CDK-PFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQFE
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-i- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
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InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR002290; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98364306; PubMed=9699150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U78857; AAC99476.1; -.
HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinase type I-like CPG16)
DCAMKL1 OR CPG16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POARREE 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 PGANAEK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily.
                                                                                                                  185
                                                                                                                                                                                          68
                                                                                                                                                                                                                                                               243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCK1 RAT
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Gaps

48;

Conservative

Matches 119;

Local Similarity

Page 11

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SYSTEM
                                                                                                                                                                                                TISSUE
   127
                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                                                                                                                                           406
                                                                                                                                                                                                                                                                                                                                                                                                                466
                                                                                                                                                                                                                         -----YKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPP 175
                                                                                                                                                                                                                                                              PRGSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRK 235
                                                                                                                                                                                                                                                                         120 -RGKE-------HMIQNEVSILRRVKHPNIVLLIEEMDVPTE--LYLVMELVKG 163
                                                                                                                                                                                                                                                                                                236 GPVME-VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGD--DG--HVK 290
                                                                                                                                                                                                                                                                                                             291 IADFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGK 350
                                                                                                                                                                                                                                                                                                                                                         277
                                                                                                                                                                                                                                                                                                                                                                                                                               338 PWVNDDG---LPENEHQLSVA----GKIKKHFNTGPKPSSTAAGVSVIATTALDK--ERQ 388
                                                                                                                                                                                                GSYLEAQAGPYATGPASHISPRAWRRPTIESH---HVAISDAEDCVQLNQ-----
                                                                                                                                                                                                                                    71 EGFQIPATITERYKVGRTIGDGNFAVVKECIERSTAREYALKIIKKSKC------
                                                                                                                                                                                                                                                                                                                                                : [||:: :| | : || | : || | : |
IGDFGLATIVDG---PLYTVCGTPTYVAPEIIAETGY---GLKVDIWAAGVITYILLCGF
                                                                                                                                                                                                                                                                                                                                                                         CPF--IDDFILALHRKIKNEPVVFPEE--PEISEELKDLILKMLDKNPETRIGVPDIKLH
                                                                                                                                                                                                                                                                                                                                                                                            278 PPFRGSGDDQEVLFDQILMGQVDFPSPYWDNVSDSAKELINMMLLVNVDQRFSAVQVLEH
                                                                                                                                                                                                                                                                                                                                                                                                              PWVTKNGEEPLPSEEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQ
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                    83;
                                                                                                                                                 ; Score 402.5; DB 1; Length 433;
; Pred. No. 3.9e-19;
69; Mismatches 179; Indels 83
       ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKG; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
                                                                         SER/PRO-RICH (BY SIMILARITY)
                                                                                                                      BY SIMILARITY.
0CESE06E152A557D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 VFRRRRNQDVRGRYKAQPA-----PPELNSESEDYSPS 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 ARREERSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS
                                                                                                   ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                   PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                               433 AA; 47680 MW;
                                                                                                                                                 15.3%;
Pfam; PF00069; pkinase; 1.
                                                                                                                                                           Best Local Similarity 21.27
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                         33
340
394
97
1112
204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                               Neurogenesis.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCK1 HUMAN
015075;
                                                                                                                                                                                      81
                                                                                                                                                                                                                         128
                                                                                                                                                                                                                                                              176
                                                                                                                                                                                                                                                                                                                                                        224
                                                                                                                                                                                                                                                                                                                                                                         351
                                                                                                                                                                                                                                                                                                                                                                                                              407
                                                                                                                      ACT SITE
SEQUENCE
                                                                                                                                                                                                      12
                                                                                          DOMAIN
NP BIND
BINDING
                                                                                                                                                Query Match
                                                                                  DOMAIN
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DCK1_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Genomic structure, chromosomal mapping, and expression pattern of human DCAMKL1 (KLAA0369), a homologue of DCX (KLIS).";
Genomics 56:179-183 (1999).
-!- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
      VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event-Alternative splicing; Named isoforms=4;
Comment-Additional isoforms seem to exist. Type A (AS and AL) and type B (BS and BL) isoforms differ respectively by the presence or absence of the doublecortin domain. An alternative splicing occurring in 3' of the mRNA produces the long (L) instead of the short (S) isoforms;
                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fetal brain;
MEDLINE=99156863; PubMed=10036192;
Sossey-Alaoui K., Srivastava A.K.;
"DCAMKL1, a brain-specific transmembrane protein on 13q12.3 that is similar to doublecortin (DCX).";
Genomics 56:121-126(1999).
"Prediction of the coding sequences of unidentified human genes. VI the complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
MEDLINE-98419166; PubMed=9747029;
Omori Y., Suzuki M., Ozaki K., Harada Y., Nakamura Y.,
Takahashi E.-I., Fujiwara T.;
Expression and chromosomal localization of KIAA0369, a putative kinase structurally related to boublecortin.";
J. Hum. Genet. 43:169-177(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 2 doublecortin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=1; Synonyms=AS;
IsoId=O15075-2; Sequence=VSP_004907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=2; Synonyms=AL;
IsoId=015075-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                               [2] SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99162404; PubMed=10051403;
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Genew; HGNC:2700; DCAMKL1.
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----PELNSESEDYSPS 728
                                                                                                           STANDARD;
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66
81
179
192
81
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58
81
179
192
427
81
192
432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P24941; 1CKP
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation
                                                                                                                                                                                                                                    STK11 OR EEK1.
                                                                                                           XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
NP BIND
BINDING
ACT SITE
MOD RES
MOD RES
MUTAGEN
KUTAGEN
SEQUENCE
                  716
                                                                                            STKB_XENLA
                                                                                                           STKB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 RAASVIPGSTSRLLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 RSTTKSPG-----PSRRSKSPASTSSVNGTPGSQLSTPRSGKSPSP-SPTSPGSLRKQR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----YKLQSEIGKGAYGVVR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 LAYNESEDRHYAMKVLSKKKLLKQYGFPRRPFPRGSQAAQGGPAKQLLPLERVYQEIAIL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRYKHPNIVLLIEEMDVPTE--LYLVMELVKGGDLFDAITSTNKYTERDASGMLYNLASA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 SSQHGGSSTSLASTKVCSSMDENDGPGEEVSEEGFQIPATITERYKVGRTIGDGNFAVVK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSEEEHCSVVEVTEGEV 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTALDKERQÜFRRRRNQDVRSRYKAQPAPPELNSESEDYSP
SSSETVRSPNSPF -> LDHGFTIKRSGSLDYYQQPGMYWI
RPPLLIRRGRFSDEDATRM (in isoform 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 KKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME-VPCDKPFSEEQARLYLRDVILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 LEYLHCOKIVHRDIKPSNILLIGD--DG--HVKIADFGVSNQFEGNDAQLSSTAGTPAFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNSVRLIP-----SWTTVILVKSMLRKRS-FGNPFEPQARREERSMSAPGNLLVKEGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPF--IDDFILALHRKIKNEPVVFPEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                             SWART; SM00537; DCX; 2.

SWART; SM00220; S TKC; 1.

PROSITE; PS050309; DC; 2.

PROSITE; PS050101; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (in isoform 3 and isoform 4).
                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
POLY-ARG.
Missing (in isoform 3 and isoform 4
Missing (in isoform 3 and isoform 4
FTIG=VSP 004905.
PASTSS -> MLELIE (in isoform 3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.2%; Score 401.5; DB 1; Length 740; 26.9%; Pred. No. 8.9e-19; ive 75; Mismatches 186; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D7B6D855099A315C CRC64;
                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASE.
ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'FTId=VSP 004906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIId=VSP 004907
                                                                                                                                                                                                                                                                                         DOUBLECORTIN 1.
                                                                                                                                                                                                                                                                                                                             SER/PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 IESH---HVAISDAEDCVQLNQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isoform 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoform 3)
                    InterPro; IPR003533; DCX.
InterPro; IPR000719; Prof. kinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                      Pfam, PF03607; DCX; 2.
Pfam, PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
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Best Local Similarity 26.9%
Matches 134; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MG(2+). SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K->I: LOSS OF ACTIVITY.
T->A: LOSS OF AUTO-PHOSPHORYLATION.
F4D98A06C52560F7 CRC64;
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InterPro; IPR000719; Ser_thr_pkina.AS.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PP00069; pkinase; I.
Swary; Sw00200; STKG; I.
PROSITE; PS00107; PROTEIN_KINASE_ATP; I.
PROSITE; PS001107; PROTEIN_KINASE_ATP; I.
PROSITE; PS00119; PROTEIN_KINASE_DM; I.
PROSITE; PS50011; PROTEIN_KINASE_DM; I.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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PHOSPHORYLATION (AUTO-)
                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine-fibreonine protein kinase 11 (EC 2.7.1.37)
protein kinase XEEK1) (Egg and embryo kinase 1).
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ATP (BY SIMILARITY).
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ilarity 35.0%; Pred. No. 8.8e-19;
Conservative 46; Mismatches 117;
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432 AA.
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PRT;
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MEDLINE=96278908; PubMed=8662877;
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Search completed: July 12, 2004, 04:51:13 Job time : 56 secs This Page Blank (uspto)

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July 12, 2004, 01:17:43; Search time 102 Seconds (without alignments) 1398.887 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
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SUMMARIES	ABB83054 AAE19161	ADE61943	ABU65068	AAE04361	AAU79458 ABU65069	ABB83055	ADE61937	ADE61941 AAY44239	ADB75228	AAM40450 AAM40449	AAM38663	AAB65659	ABG61855	ADB75230	ADC99093	AAM38664	AAM25244
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ABB66416	ABU11714	AAM25471	ABR52943	ABB78798	ABR40710	AAR40842	AAB03425	ABR40719	AAB03419	ABR40713	AAB03421	ABR40715	AAB03423	ABR40717	ABB78797	ABR44015	AAG70854	AAB03417	ABR40709
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33.4	24.6	23.2	21.5	20.0	17.2	16.6	16.3	16.3	16.3	16.3	16.3	16.3	16.2	16.2	16.2	16.2	16.2	16.1	16.1
881	648	611	266	526	452	436.5	430.5	430.5	429.5	429.5	428.5	428.5	428	428	427	426.5	426.5	424.5	424.5
56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESU	RESULT 1	
	83054	standard; protein; 505 AA.
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A Y	ABB83054;	
ž E	27-AUG-2002 (Fi	(first entry)
¥ 2	Direct Court of the Court	
ž ž	numan kinase am.	sequence.
X.	Human, kinase protein;	rotein; calcium/calmodulin-dependant protein kinase; eye;
ž	recimontascoma;	
s ×	Homo sapiens.	
표	Key	Location/Qualifiers
FT	Region	2629
H H		/label= casein_kinase_II_phosphorylation_site
1 6	keg1on	58bU /lahal- protein kinase C phoephorylation site
i E	Region	
FT		/label= protein kinase C phosphorylation site
FT	Region	7174
FT		/note= "cAMP- and cGMP-dependant protein kinase
F		phosphorylation site"
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FT	in factor	/label= casein kinase II phosphorylation site
FI	Region	100102
FT		/label= protein_kinase_C_phosphorylation_site
다! H	Region	105108
FI		/note= "cAMP- and cGMP-dependant protein kinase
T L	Region	phosphoryractom sine
FT	104604	/label= casein kinase II phosphorylation site
FT	Region	134. 157
FT		/note= "protein kinase ATP-binding region signature"
	keg1on	14/130 /label- N-glycosylation eite
FT	Region	140162
F		/label= protein_kinase_C_phosphorylation_site
I E	kegion	178183 /label= N-mvristovlation site
FT	Region	271283
E E		/note= "serine/threonine protein kinase active-site
F	Region	signature" 326331

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(HK), that has homology to members of the calcium/calmodulin-dependent protein kinase kinase subfamily. The mechanism of action of the protein of the invention is that of a kinase modulator. The human kinase of the invention is useful for creating a pharmaceutical composition for treating a disease or condition mediated by the human kinase. HK is also useful to provide a target for diagnosing a disease or predisposition to disease mediated by HK, and is also useful in pharmacogenic analysis. HK is useful for treating a disorder characterised by absence of inappropriate or unwanted expression of HK, also as an immunogen to raise antibodies by administering HK to a mammalian organism e.g. rat. rabbit or mouse. Nucleic acids of the invention are useful as hybridisation contibodies for mRM, transcript/companion of the invention are useful as hybridisation expressing a native HK are useful for assaying compounds that stimulate or inhibit HK function. Nucleic acids of the invention are also useful for preducing transcript/cDNA and genomic DNA. Recombinant host cells expressing transcript/cDNA and genomic assaying compounds that stimulate or inhibit HK function. Nucleic acids of the invention are also useful for preducing transgenic animals. Experimental data indicates that kinase proteins of the present invention are expressed in humans in the eye (retinoblastomas) and brain. The current sequence represents the amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wel peptide designated as human kinase useful as target for diagnosing disease or predisposition to the disease mediated by the peptide.
                                                                       /note= "wild-type Glu is replaced by Gly as a result of
an SNP (single nucleotide polymorphism) in the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated peptide designated human kinase
                                                                                                                                                                                                                                                                                                     cGMP-dependant protein kinase
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/label= casein_kinase_II_phosphorylation_site
425. .428
/label= casein_kinase_II_phosphorylation_site
                 330. 332
/label= protein_kinase_C_phosphorylation_site
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/label= protein_kinase_C_phosphorylation_site
455. .458
/note= "cAMP- and cGMP-dependant protein kinas
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 N-myristoylation site
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2000US-0247031P.
2000US-00729995.
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                                                     Misc-difference
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06-DEC-2000;
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DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ 180
                                                                                                                                 AAQGGPAKQLLPLERVYQEIAILKKCDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME 240
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                                                                                                                                                                                                                                                                                                            Human; kinase polypeptide; PKIN-19; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic;
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                LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE
                                                                                                                AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME
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2000US-0222112P.
2000US-0222831P.
2000US-0224729P.
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28-JUL-2000;
04-AUG-2000;
11-AUG-2000;
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Length 505;

100.0%; Score 2634; DB 5; 100.0%; Pred. No. 2.8e-236;

0; Mismatches

Matches 505; Conservative

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Best Local Similarity

Query Match

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The present invention relates to an isolated human kinase polypeptide

(PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is

useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
lymphoma, melannoma), an immune disorder (e.g., acquired immunodeficiency
syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's

disease, rheumatoid arthritis, psoriasis, Cushing's syndrome), a

cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial

cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial

infarction), and a lipid disorder (e.g., fatty liver, cholestasis,

Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of

drug screening techniques and to analyse the proteome of a tissue or cell

type. PKIN is useful for creating knockin humanised animals or transgenic

animals to model human diseases, in somatic or germline gene therapy, to

generate a transcript image of a tissue or cell type, for detecting

differences in the chromosomal location due to translocation, inversion,

cycle probes for mapping naturally occurring genomic sequences. PKIN is useful

conthern or northern analysis, dot blot or other membrane-based

chechnologies, in PCR technologies, in dipstick, pin, multiformat enzyme

linked immunosorbent (ELISA)-like assays and in microarrays utilising

cycles for mapping naturally occurring denomic sequences. PKIN is expression. The
                                                                                                                                                                                                                                                                                                New human kinase polypeptide, useful in diagnosis, prevention and treatment of cancer, immune disorder, growth and developmental disorder, cardiovascular disorder and lipid disorder.
                                                                    Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia NK;
Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding
ott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 168-170; 196pp; English.
INCYTE GENOMICS INC.
                                                                                              Patterson C, Ramkumar J, C
Tribouley CM, Bandman O, N
Yao MG, Elliott VS, Recipo
Tang YT, Xu Y, Walsh RT,
                                                                                                                                                                                                                            WPI; 2002-206083/26.
                                                                      Yue H,
                    THORNTON M.
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                                                                         Thornton M,
(INCX-)
                       THOR/)
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Sequence 505 AA;

ö LHRKIKNEPVVFPEEPEISEELKOLILKOALDKNPETRIGVPDIKLHPWYTKNGEEPLPSE 420 AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLIRKGPVME 240 241 VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300 LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120 120 121 DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ 180 AAQGGPAKQLLPLERVÝQEIAILKKLDHVNVÝKLIEVLDDPAEDNLÝLVFDLLRKGPVME 240 VPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300 EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360 EGNDAQLISSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360 121 DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ 180 9 1 MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARASVIPGSTSR 60 1 MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR Gaps . 0 99.7%; Score 2626; DB 5; Length 505; 99.8%; Pred. No. 1.6e-235; ive 0; Mismatches 1; Indels 0 Best Local Similarity 99.8 Matches 504; Conservative 301 61 181 181 241 361 Query Match 셤 원 원 g 8 δ g à g δ ð

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comparison of the mucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a stray, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that completes its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition (e.g. spinal segmental nerve injury (CMI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of
                                                                EEHCSVVEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEDQARREERSMSAPGNL 480
361 LHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE 420
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                                         EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
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                                                                                                                                                                                                                                                                                                                                                                                                          Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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                                                                                                                                               481 LVKEGFGEGGKSPELPGVQEDEAAS 505
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                              DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPPRGSQ
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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                                                                                                     Length 505;
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                                                                                                    Query Match 99.7%; Score 2626; DB 7;
Best Local Similarity 99.8%; Pred. No. 1.6e-235;
Matches 504; Conservative 0; Mismatches 1;
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01-NOV-2001; 2001US-0346382P.
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising ne nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a ckit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the polynetides or manimal of one or more of the polypeptides or their antibodies. The polynucleotide or more control or polynucleotides or their antibodies. The polynucleotide or more conformed to manimal end a pharmaceutical composition compound useful in treating pain and a pharmaceutical composition comprising the one or more conformation and spared nerve injury (Chung), chronic constriction injury (Ctl) and spared nerve injury (SNI) in an animal end or this patent did not form part of the printed the sequence data for this patent did not form part of the printed to the sequence data for this patent did not form part of the printed the patent of the printed the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed the printed the printed to the control or the control or the control or the control or the control or the control or the control or the control or the control or the control or the control or the control or the contro
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                                                                                               Costigan M;
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                    GEN HOSPITAL CORP. BAYER AG.
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                                                                                            Woolf C, D'urso D,
                                                                                                                                             WPI; 2003-268312/26
                                                                                                                                                                       GENBANK; NP 115670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polymucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-ABZ1066) or their mature procein coding portion, active domain coding protein or complementary sequences. The polymucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABE68902-ABP69849) are useful as molecular weight maging, screening and diagnostic assays and for treating cellimaging, screening and diagnostic assays and for treating cellimaging, screening and diagnostic assays and for treating cellimaging, screening and diagnostic and for the scleens; or Alzheimer's diseases (multiple sclerosis, contacted as diseases, multiple sclerosis, diabetes, lupus) genetic disorders, wound, burns, incision, ulcers, liver the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                     Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
               420
                                        480
                                                                 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides comprising sequences assembled from expressed sequence tags (EGTs), useful for treating cell-proliferative, neurodegenerative, autonimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders.
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                                                   LHRKIKNEPVVPPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE
                                    EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, F
Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
f, Wang J, Wang D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; SEQ ID NO 1381; 1012pp + Sequence Listing; English.
                                                                                          505
                                                                                                      LVKEGFGEGGKSPELPGVQEDEAAS
                                                                                                                                                                                 ABP69334 standard; protein; 582 AA
                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 1381.
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Pred. No. 8.9e
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08-MAR-2001; 2001US-0274394F.
08-MAR-2001; 2001US-0274381F.
09-MAR-2001; 2001US-0274469F.
12-MAR-2001; 2001US-02746469F.
13-MAR-2001; 2001US-027535F.
                                     99.4%;
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                                                                               503; Conservative
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                                                             Similarity
Sequence 582 AA;
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1; Page 139; 1103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVX polypeptides and polynucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Padigaru M, Spytek KM, Tw, Gorman L, Zerhusen BD, Gusev V, Ji W, Gorman L, Patturajan M, Gangolli E, Vernet CAM, Guo X, Patturajan M, Gangolli E, Malyankar UM, Gerlach L. Casman SJ, Malyankar UM, Gerlach M, E. Eurgess C, Leite M,
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2001US-0299310P
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2001US-0312909P
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2001US-03303B1P.
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2001US-03323112P.
2001US-0332311P.
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2001US-0281194P.
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N-PSDB; ABX97035.
                               19-MAR-2001;
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27-SEP-2001;
18-OCT-2001;
31-OCT-2001;
14-NOV-2001;
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14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
21-NOV-2001;
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03-DEC-2001;
                        16-MAR-2001;
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                      cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, athereosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABU65041-ABU65218 represent the NOVX polypeptides encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
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This invention describes novel human NOVX polypeptides which
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                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.1%; Score 2611; DB 5; Best Local Similarity 99.4%; Pred. No. 3.9e-234; Matches 502; Conservative 0; Mismatches 3;
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WO200138503-A2

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ANU03501-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polymucleotides conciding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with imperopriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disease (e.g. schizophrenia), neurodegenerative disorders (e.g. dispetes), and reproductive disorders (e.g. infertility).

Additionally, polymucleotides encoding protein kinases may be used for gene therapy and as DNA probbes in disapnostic assays. The protein kinase polypeptides may be used as antiquens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections.
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                                                                                                                                                                                                                                                  Nucleic acids encoding human kinase polypeptides, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2595; DB 4; Length 513;
Pred. No. 1.3e-232;
0; Mismatches 1; Indels 10
                                                                                                                                                           Sudarsanam S,
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                                                                                                                                                                                                                                                                                                               Claim 7; Fig 2; 433pp; English.
                                                                                                                                                           Manning
                                                           22-NOV-2000; 2000WO-US032085.
                                                                                          99US-0167482P
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Matches 503; Conservative
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Clary D;
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                                                                                         24-NOV-1999;
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                                                                                                                                                                        Flanagan P,
                             31-MAY-2001
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Best Local 8
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NGEEPLPSEEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREE 471 Human kinase; PKIN-2; therapy; immune disorder; Addison's disease; AIDS; acquired immune deficiency syndrome; growth and developmental disorder; arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinome; leukaemia; cardiovascular disease; myocardial infarction; hypertension; lipid disorder; cancer; fatty liver; cholestasis; transgenic animal; gene therapy; antiallergic; antiasthmacic; antithyroid; dermatological; antidabetic; nephrotophic; antiulcer; antiarthritic; antirheumatic; antiposiatic; neuroprotective; cytostatic; hepatotrophic; osteopathic; vasotropic; antianginal; anorectic. Novel human kinase proteins (PKIN) useful for diagnosing, treating, preventing immune disorders, cardiovascular diseases and disorders affecting growth and development associated with abnormal expression of 193. .500
/note= "ATP/GTP-binding site motif A (P-loop)" Reddy 'note= "Eukaryotic protein kinase domain" "Tyrosine kinase catalytic domain" /note= "Tyrosine kinase catalytic domain" Lu DAM, "Tyrosine kinase catalytic 505 130. .408 /note= "Protein kinase domain" 1. .127
/note= "Kinase protein beta" Au-Young J, RSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS Claim 1; Page 104-105; 128pp; English Location/Qualifiers AAE04361 standard; protein; 513 AA Burford N, P, Khan FA; 23-DEC-1999; 99US-0172066P. 14-JAN-2000; 2000US-0176107P. 21-JAN-2000; 2000US-0177731P. 20-DEC-2000; 2000WO-US035304 28-JAN-2000; 2000US-0178573P (INCY-) INCYTE GENOMICS INC (first entry) .417 .330 273. .291 342. .364 'note= 'note= Human kinase (PKIN)-2. Baughn MR, Yao MG, Lal WPI; 2001-418059/44. N-PSDB; AAD08635. WO200146397-A2 Homo sapiens. Binding-site 04-SEP-2001 28-JUN-2001. 412 472 Yang J, 'ne H' Region Domain Domain Domain Domain Domain AAE0436. RESULT 셤 Š qq LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120 171 DCVQLNQYKLQSEIGKVGLTDAYLQGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFP 180 RRPPPRGSQAAQGGPAKQLLPLERVYQEIAILKKKLDHVNVVKLIEVLDDPAEDNLYLV-D 239 231 291 ADFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGRALDVWATGVTLYCFVYGKC 359 PFIDDFILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTK 411 ADFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKC 351 9 9 Gaps 10; Martinez R;

The invention relates to novel human kinase proteins (PKIN) and nucleic acid molecules encoding them. PKIN is useful for identifying compounds that modulates its activity. PKIN cDNA is useful for assessing toxicity of a test compound. PKIN and its CDNA are useful for diagnosis, prevention and treatment of immune disorders such as acquired immune deficiency syndrome (AIDS), Addison's disease, anaemia, adult respiratory defisitess syndrome, allergies, amyloidosis, psoriasis, autoimmune haemolytic anaemia, autoimmune thyroiditis, molitiple sclerosis, asthma, osteoarthritis, osteoporosis, rheumatoid arthritis, ulcerative colitis and diabetes mellitus; growth and developmental disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), and myelofibrosis; cancers such as adenocarcinoma and leukaemia, cardiovascular diseases such as adenocarcinoma on hypertension; and lipid disorders such as fatty liver and cholestasis. PKIN cDNA is useful to detect upstream sequences such as promoters and regulatory elements, for creating knock in or knock out in humanised animals or transgenic animals to model human disease and for somatic or germaine gene therapy for treating the above mentioned disorders. The present sequence is human kinase (PKIN)-2

Sequence 513 AA;

419 351 359 471 479 61 LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120 120 171 DCVQLNQYKLQSEIGKVGLTDAYLQGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFP 180 231 239 299 411 291 9 1 MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR 181 RRPPRGSQAAQGGPAKQLLPLERVYQETAILKKLDHVNVVKLIEVLDDPAEDNLYLV-D 240 LLRKGPVMEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKI 352 PFIDDFILALHRKIKNEPVVFPREPRISEELKDLILKMLDKNPETRIGVPDIKLHPWVTK 360 PFIDDFILALHRKIKNEPVVFPEEPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTK 412 NGEEPLPSEEEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREE 121 DCVQLNQYKLQSEIGK-----GAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFP 172 RRPPPRGSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFD ADFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKC 300 ADFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKC LLRKGPVMEVPCDKPFSEEQARLYLRDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKI Gaps 10; Query Match

98.5%; Score 2595; DB 4; Length 513;
Best Local Similarity 97.9%; Pred. No. 1.3e-232;
Matches 503; Conservative 0; Mismatches 1; Indels 10 RSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS 505 RSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS 232 472 480 292 셤 g g g ŏ ð ò ð ò q ð à g ò 셤 ð 셤

AAU79458 standard; protein; 561 AA. 15-JUL-2002 (first entry) Human novel kinase 16002. AAU79458; RESULT 9 AAU79458 RXHXRX

New human transferase protein for diagnosing and treating disorders e.g. cancer, Alzheimer's disease, anorexia, diabetes and to identify modulators for therapeutic use. carcinoma; tumour; adenocarcinoma; heematopoietic neoplastic disorder; leukaemia; lymphoma; brain disorder; cerebral ischaemia; infection; meningitis; brain abscess; acquire immunodeficiency syndrome; obesity; AIDS-related myopathy; prion disease; Alzheimer's disease; diabetes; Parkinson's disease; Huntington's disease; motor neurone disease; metabolic disorder; anorexia nervosa; pain; inflammation; ischaemia; irritable bowel syndrome; hart disorder; myocardial infarction; blood vessel disorder; atherosclerosis; bone metabolism disorder; cancer; enzyme; 16002; kinase; cellular proliferative disorder; osteoporosis; haematopoietic disorder; arthritis. Meyers RA, Silos-Santiago I; 03-AUG-2001; 2001WO-US024601. 01-SEP-2000; 2000US-0229299P. (MILL-) MILLENNIUM PHARM INC. WPI; 2002-351781/38. N-PSDB; ABK49563 WO200220800-A2 Homo sapiens 14-MAR-2002

Claim 4; Fig 16; 143pp; English.

The invention relates to an isolated human kinase polypeptide encoded by the DNAs designated 16658, 14223 and 16002 included are a host call comprising the DnAs designated 16658, 14223 and 16002 included are a host call comprise to the DNA, an antibody which selectively binds to the novel kinase, a mathod for producing the novel kinase comprising culturing the host call and recovering the sample with a compound which selectively hydridises to the DNA and determining whether the compound has bound and determining whether the compound has bound and determining whether the compound has bound to and/or modulate the protein comprising contacting the protein with a test compound and determining whether the compound has bound to and/or modulated the function of the protein (the modulators may be a small molecule, a peptide, a protein and antibody or a fragment of the full length protein).

The nucleic acids, proteins, identified modulators and antibodies are useful in the diagnosis, monitoring and treatment of a wide range of diseases and disorders (many examples of which are listed in the specification) including callular proliferative disorders (e.g. cancers of the lung and breast, carcinomas, tunnurs, adenocarcinomas, brain and nerve tissue disorders (e.g. carebral ischaemia, infections such as meningitis, brain abscress, acquired immunodeficiency syndrome (AIDS) - crelated myopathy, prion diseases, and motor neurone disease) metabolic calsorders (e.g. associated with infection, inflammation ischaemia, irritable bowel casorders (e.g. associated with infection, inflammation ischaemia, irritable bowel casorders (e.g. atherosclerosis), disorders of bone metabolism (e.g. atherosclerosis) disorders of bone metabolism (e.g. acceporosis) and haemacopoletic disorders of bone metabolism (e.g. atherosclerosis) disorders of bone metabolism (e.g. atherosclerosis) disorders of bone metabolism (e.g. atherosclerosis) disorders of bone metabolism (e.g. atherosclerosis) disorders of bone metabolism (e.g. atherosclerosis) disorders

Sequence 561 AA;

Gaps ;0 Length 561; Indels Score 2591; DB 5; Pred. No. 3.4e-232; 0; Mismatches 2; 98.48; Best Local Similarity 99.6%; Matches 497; Conservative Query Match

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Padigaru M, Sp
Zerhusen BD, G
Patturajan M,
Fernandes ER,
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30-MAY-2001; 2
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31-MAY-2001; 2
31-MAY-2001; 2
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14-NOV-2001; 2
21-NOV-2001; 2
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22-MAR-2001; 23-MAR-2001; 25-MAR-2001; 27-MAR-2001; 27-MAR-2001; 28-MAR-2001; 28-MA
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19-JUN-2001;
10-JUL-2001;
31-JUL-2001;
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10-SEP-2001;
12-SEP-2001;
27-SEP-2001;
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                                          EEHCSVVEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
                                                                                DCVQLNQYKLQSE1GKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPRGSQ
                                                                                                                                                      VPCDKPFSEEQARLYLRDVILGLEYLHCQXIVHRDIKPSNLLLGDDGHVKIADFGVSNQF
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MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
                          LLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE
                                                                                                                                        AAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDLLRKGPVME
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Mypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
human.
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2001US-0274194P.
2001US-027432P.
2001US-0274322P.
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2001US-0275579P.
2001US-0275601P.
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09-MAR-2001;
12-MAR-2001;
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13-MAR-2001;
13-MAR-2001;
14-MAR-2001;
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19-MAR-2001;
20-MAR-2001;
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-MAR-2001;
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21-MAR-2001;
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This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
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Alsobrook JP;
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Kekuda R;
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2001US-027934P
2001US-0279344P
2001US-027938B
2001US-0280233P
2001US-0280233P
2001US-0280802P
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2001US-0283675P.
2001US-0287424P.
2001US-0288066P.
2001US-0288342P.
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2001US-029489P
2001US-0299303P
2001US-0299310P
2001US-0304344P
2001US-03041344P
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2001US-0330380P.
2001US-0335301P.
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2001US-0291099P.
2001US-0291240P.
2001US-029448SP.
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2001US-0318462P.
2001US-0318770P.
2001US-0325430P.
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2001US-0332271P.
2001US-0332272P.
2001US-0333184P.
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2001US-0332094P.
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2001US-0338092P.
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Gusev V,
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Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L; Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R; Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V; Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Ande: Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobre Lepley DM, Rieger DK;
08-MAR-2001; 2001US-0274101P.
08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-0274194P.
08-MAR-2001; 2001US-0274194P.
12-MAR-2001; 2001US-027521B.
13-MAR-2001; 2001US-027521B.
13-MAR-2001; 2001US-027521B.
13-MAR-2001; 2001US-027521B.
13-MAR-2001; 2001US-027521B.
14-MAR-2001; 2001US-027521B.
15-MAR-2001; 2001US-027521B.
16-MAR-2001; 2001US-0277321P.
20-MAR-2001; 2001US-0277321P.
20-MAR-2001; 2001US-0277321P.
21-MAR-2001; 2001US-0277321P.
22-MAR-2001; 2001US-0277321P.
23-MAR-2001; 2001US-0277321P.
24-MAR-2001; 2001US-0277321P.
25-MAR-2001; 2001US-0277331P.
27-MAR-2001; 2001US-0277331P.
27-MAR-2001; 2001US-0277331P.
27-MAR-2001; 2001US-0279344P.
27-MAR-2001; 2001US-0279348P.
27-MAR-2001; 2001US-0279331P.
27-MAR-2001; 2001US-0299310P.
27-MAY-2001; 2001US-0299303P.
27-MAY-2001; 2001US-0299303P.
27-MAY-2001; 2001US-03993184P.
27-MAY-2001; 2001US-0339303P.
27-MAY-2001; 2001US-0339303P.
27-MAY-2001; 2001US-0339303P.
27-MAY-2001; 2001US-03393092P.
27-MAY-2001; 2001US-0339092P.
27-MAY-2001
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    180
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                                                                                                                                                                                                            LLPARPSISARKLSLQERPAGSYLEAQAGPYATGPASHISPRAWRRPTIESHHVAISDAE 120
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 asthma. The products of the invention can be used for gene therapy or a vaccine. ABU65041-ABU65218 represent the NOVX polypeptides encoded b ABX97008-ABX97185
                                                                                                                                                                                                                                                                                                                                               1 MEGGPAVCCODPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
                                                                                                                                                                   1 MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDPPPRARAASVIPGSTSR
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                                                                                                                       Gaps
                                                                                                                       38;
                                                                                         Length 543;
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                                                                                         98.1%; Score 2585; DB 5;
92.4%; Pred. No. 1.2e-231;
iive 0; Mismatches 3;
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                                                                                                         Local Similarity 92.4
nes 502; Conservative
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                                                             Sequence 543 AA;
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, Anderson D; Alsobrook JP;

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calcium/calmodulin-dependant
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13-NOV-2000; 2000US-0247031P.
06-DEC-2000; 2000US-00729995.
                                                                                                         19-SEP-2001; 2001WO-US029161.
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472; Conservative
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                                    Rattus norvegicus
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Best Local Si
Matches 472;
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                                                                                                                 This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomypeathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine.
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                                     treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGNDAQLSSTAGTPAFMAPEAISDSGQSFSGK-LDVWATGVTLYCFVYGKCPFIDDFILA
                                  NOVX polypeptides and polynucleotides, useful for preventing or treatiand sorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
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7
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                                                                                                                                                                                                                                                                  Score 2560; DB 5;
Pred. No. 2.2e-229;
2; Mismatches 5;
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                                                                                              Claim 1; Page 139; 1103pp; English.
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                                                                                                                                                                                                                                                                             Best Local Similarity 98.2
Matches 496; Conservative
 2002-723332/78.
                                                                                                                                                                                                                  ABX97008-ABX97185
            N-PSDB; ABX97034
                                                                                                                                                                                                                                          Sequence 503 AA;
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The invention relates to an isolated peptide designated human kinase

(HK), that has homology to members of the calcium/calmodulin-dependent
protein kinase kinase subfamily. The mechanism of action of the protein

of the invention is that of a kinase modulator. The human kinase of the

continuous a useful for creating a pharmaceutical composition for

treating a disease or condition mediated by the human kinase. HK is also

useful to provide a target for diagnosing a disease or predisposition to

disease mediated by HK, and is also useful in pharmacogenic analysis. HK

is useful for treating a disorder characterised by absence of

inappropriate or unwanted expression of HK, also as an immunogen to raise

nutbodies by administering HK to a mammalian organism e.g. rat. rabbit

or mouse. Nucleic acide of the invention are useful as hybridisation

probes for mRNA, transcript/cDNA and genomic DNA. Recombinant host cells

expressing a native HK are useful for assaying compounds that stimulate

or inhibit HK function. Nucleic acide of the invention are also useful

for producing transgenic animals. Experimental data indicates that kinase

proteins of the present invention are expressed in humans in the eye

creating sequence related to to kinase protein of the invention, appearing as

caid sequence related to to kinase protein of the invention, appearing as
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protein kinase; eye;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide designated as human kinase useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanders
                                      retinoblastoma; brain; kinase modulator
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The invention discloses a composition comprising two or more isolated rat or the invention discloses or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector; a method for identifying a mucleotide sequence which is differentially regulated in an animal subjected to pain and a ckit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in a mainal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the compound or small molecule that regulates the cativity in an animal of one or more of the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating
EGNDAQLSSTAGTPAFMAPEALSDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILA 360
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                                                                                                                                                                                                                                                                                                             Rat, pain, neuronal tissue, gene therapy; spinal segmental nerve injury, chronic constriction injury, CCI; spared nerve injury; SNI; Chung.
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                                361 LHRKIKMEAVVFPEEPEVSEBLKDLILKMLDKNPETRIGVSDIKLHPWYTKHGEEPLPSE
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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GENBANK; AAB46910.
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pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                          DCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLSKKKLLKQYGFPRRPPRGSQ 180
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93.5%; Pred. No. 8.5e-221;
iive 11; Mismatches 22;
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                                                                                                                                                                                      Sequence 505 AA;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                         The invention discloses a composition comprising two or more isolated rat or human polymuclectides or a polymuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymuclectide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the cutivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating complaints in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating complaints its activity is useful for preparing a medicament for treating collypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating collypeptides or their antibodies. The polymucleotide or the compound that injury (CCI) and spared nerve injury (SNI) in an animal (e.g. spin) ed.g. spin (e.g. spin) and pared nerve injury (SNI) in an animal (e.g. spin) ed.g. spin (e.g. spin) sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the print of the protein (or the protein in the sequence of the sequence date for this patent did not form attrict form with the sequence da
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                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                           Costigan M;
                                                                                                                                            Befort K,
                                                                                                                                                                                                                                                                    Claim 1; Page; 1017pp; English
                             14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
14-AUG-2002; 2002WO-US025765.
                                                                                          (GEHO ) GEN HOSPITAL CORP
(FARB ) BAYER AG.
                                                                                                                                         Woolf C, D'urso D,
                                                                                                                                                                        2003-268312/26.
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Cell signalling protein-2; CSIGP-2; cell proliferation; arteriosclerosis; inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS; Addison's disease; multiple sclerosis.
                                                                                                                                                                                                                                  301 EGNDAQLSSTAGTPAFMAPEAISDTGQSFSGKALDVWATGVTLYCFVYGKCPFIDEYILA 360
                                                                                 LHRKIKNEPVVFPEEPEISEELKULILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSE
                                                                                                                  EEHCSVVEVTEGEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNL
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462
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/label= Signature_sequence
                                                                                                                                                                                                                                                                                                                                               LVKEGFGEGGKSPELPGVQEDEAAS 505
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CDNA obtained from Instructure of 640521 of BRSTNOT03 library. It is expressed in reproductive, nervous and developmental tissues and is found to be homologous to Ca2+fcalmodulin-dependent protein kinase kinase. Fragments of CSIGP encoding nucleic acid can be used as hybridisation probe for detecting CSIGP related sequences or allelic variants. Recombinant CSIGP can be produced in host cells by transforming them with probe for detecting CSIGP related sequences or allelic variants. Recombinant CSIGP can be produced in host cells by transforming them with the treatment of cell proliferative and inflammatory disorders associated with decreased or increased CSIGP expression. CSIGP is used in the diagnosis, prevention and treatment of cell proliferative disorders like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders like AIDS, Addison's disease, multiple sclerosis, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence is cell signalling protein-2 (CSIGP-2) encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 EADGGPEPTRNGVDPPPRARAASVIPGSTSRLLPARPSLSARKLSLQER-----PAGSYL
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                                                                                                                                                                                                                                                                                                                                                                                                                     Human cell signaling proteins useful for, e.g. diagnosing cell proliferative and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                      Patterson
                             note= "Potential phosphorylation site"
'note= "Potential phosphorylation site"
                                                                  'note= "Potential phosphorylation
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                                                                                                                                                                                                                                                                                   (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                    Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-086432/07.
N-PSDB; AAZ29223.
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Best Local Similarity
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            Modified-site
                                             Modified-site
                                                                                                                                 WO9958558-A2
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26-AUG-1998;
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Baughn MR,
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completed: July 12, 2004, 04:50:08

: 106 secs

Job time

Search

379 SEELKDLILKMLDKNPETRIGVPDIKLHPWVTKNGEEPLPSEEEHCSVVEVTEGEVKNSV 438

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1518)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Rerriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, W. D. and Cargill, D. R. Lu, F., Murphy, B., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY416154 15-BC.
Homo sapiens CAMKKI gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
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14671302
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                  BM805189
BU552890
                                               BG705317
BQ932168
BQ277875
BQ277875
BG396486
BX328136
BX328136
BX328136
BX321613
BG701043
BIR19446
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AK044660
BM950087
BU902211
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BG294573
BU671280
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BM087446
BI225425
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BY735290
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BM150448
BE562166
BU420206
BU367227
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BM952005
BE887687
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BX350723
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BX328334
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AY416154
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AUTHORS
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AUTHORS
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KEYWORDS
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                              27513289 segs, 14931090276 residues
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AL582916 AL582916 BM150448 TCBAP1D10 BE562166 601346127 BU420206 603399723 BX488903 DKFZp686M BM95207 UI-M-EHO-BE887687 601511851 BM952005 UI-EHO-BE887687 601511851

BX350723 RPCI-11-4

BX328334

CDA32-A01

CD498154 (BX350723 B AQ629789 BX328334 I GSS 17-DEC-2003

AK032070 Mus muscu AK044660 Mus muscu BM950807 ULM-EH0p BU902211 AGENCOURT BI756153 60309105 BU671280 NISC_Ir07 BU571280 NISC_Ir07 BU54678 60319135 BM087446 500218 MA BI225425 602950187 BU112704 603141003 CB712291 AMCNUC:N BY735290 BY735290

BX328136 BX328136 BQ571613 UI-M-FC0-BG701043 602682056 BI819446 603034234

BX459685 602459214

BQ277875 PBX459685 EBG396486

BQ932168 AGENCOURT BQ277875 AGENCOURT

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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1518)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Addms, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY416156 1518 bp DNA linear GSS 17-DEC-
Mus musculus CAMKK1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
                                                                                            GAGGGGAACGACGCTCAGCTGTCCAGCACGGCGGAACCCCCAGCATTCATGGCCCCCGAG
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Science 302 (5652), 1960-1963 (2003)
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2 (bases 1 to 1518)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
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VERSION
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SOURCE
ORGANISM
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA. This sequence was made by sequencing genomic exons and ordering them based on alignment.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                        Location/Qualifiers
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/gene="CAMKK1"
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Best Local Similarity 99.7%;
Matches 1511; Conservative
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Pan troglodytes CAMKKI gene, VIRTUAL TRANSCRIPT, partial sequence,
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Pan troglodytes
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Pan.
1 (bases I to 1445)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Adams, M.D. and Cargill, M.
Inferting nonneutral evolution from human-chimp-mouse orthologous gene trios
                                            CTGGGCCTCGAGTACTTGCACTGCCAGAAGATTGTCCACAGGGACATCAAGCCATCTAAC
                                                                                                                                                                                GAGGGGAACGACGCTCAGCTGTCCAGCACGGCGGGAACCCCAGCATTCATGGCCCCCGAG
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                        CTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAAC
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Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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/gene="CAMKK1"
/locus_tag="HCM5796"
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AL539375 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF033X017 5-PRIME, mRNA sequence.
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                  GTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCCTCTACCTGCGGACGTCATC
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12868532.
Contact: Genoscope
Genoscope - Centre National de Sequencage
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                                 /clone_lib="Roca" sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
was printed, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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BP 191 91006 EVRY cedex - France
Email: seqret@genoscope.uns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8786.r For
more information about this cluster, see
thtp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODF033AH090pl&cluster=8786.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF033AH09QP1.
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/organism="Homo sapiens"
/mol_type="mkna"
/db_xref="taxon:9606"
/clone="CSODF033YO17"
/tissue_type="FETAL BRAIN"
                                                                                                                                                                    Location/Qualifiers
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 9100 EVRY cedex - Advision of
Invitrogen. This sequence belongs to sequence cluster 8786.r For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODK012BD11QP1&cluster=8786.r. Contact :
Feng Liang Email : fliang@llfetech.com VRL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODK012BD11QP1.
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BX401350 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CSODK012YG22 5-PRIME, mRNA sequence.
BX401350
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TGAGGACAACCTCTATTTGGTGTTTGACCTCCTGAGAAAGGGGCCCCGTCATGGAAGTGCC
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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mRNA sequence

5-PRIME,

clone CS0DD001YE15

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                        Gaps
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   Length 1034;
                        Indels
                        4;
  Score 892.4; DB 13
Pred. No. 1.1e-186;
                      2; Mismatches
58.9%;
                      904; Conservative
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Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191006 EVRY cedex - France
Bmail: seqret@Genoscope.ns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8786.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi'sseq-CS0DD001AC080plscluster=8786.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DD001AC08Qpl.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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                                                                                                                                                           Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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Pred. No. 4.8e-186;
6; Mismatches 2;
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                       GI:30628440
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562

BX395129

1201 bp mRNA linear EST 13-MAY-2003
BX395129 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens

BX395129 LOCUS DEFINITION

RESULT

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CAACC--AGTTTGAGGGGAACGACGCTCACTGTCC---AGCACGGCGGGAACCCCAGCA 945
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Enkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
El (Bases I to 1096)
I (Bases I to 1096)
I (Bases I to 1096)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Right quality sequence stop: 633.
                                                                                                                                                                                                                                                                                                                                                                                                                                             BM805189 1096 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6499735 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728398
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                  AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGGTCCCAG
                                                              GCTGCCCAGGGAGGACCAGCCAAGCAGCTGCTGCCCCTGGAGCGGGTGTACCAGGAGATT
                                                                                                              GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC
                                                                                                                                                   CCAGCTGAGGACAACCTCTATTTGGTGTTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAA
                                                                                                                                                                 CCAGCTGAGGACAACCTCTATTTGGTGTTTGACCTCCTGAGAAAGGGCCCGTCATGGAA
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/lab_host="DH108"
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/db_xref="taxon:9606"
/clone="IMAGE:5728398"
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cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
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Tissue Procurement: Miklos Palkevits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAMI0725 row: a column: 07

High quality sequence stop: 769.
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1 (Dases 1 to 880)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                AGCACGGCGGGGAACCCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCCGGCCAGAGC
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/wol_type="mRNA"
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/db_txef="texon:9606"
/clone="IMAGE:6576737"
/tissue_type="textocarcinoma, cell line"
/lab_host="IMH_MGC_109"
/clone_lib="NIH_MGC_109"
/clone_lib="NIH_MGC_109"
/clone_lib="NIH_MGC_109"
/clone_lib="NIH_MGC_109"
/clone_lib="Organ: ovary; Vector: pOIB7; Site_1: EcoRI; Site_2:
/hote="Organ: ovary; Vector priming. Directionally cloned
into EcoRI/ANOI sites using the following 5: adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be http://image.lln.gov 1 column: 17
High quality sequence stops 658.
Location/Qualifiers
1. 939
Location/Qualifiers
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978 CAACCCANTITGAAGGGGAACCACGCTCAACTGTTCCAGAACGGGGGGGAAACCCCCACCA 1037
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AGENCOURT 10373297 NIH_MGC_109 Homo sapiens cDNA clone
MAGE:6576737 5', mRNA sequence.
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Matches 815; Conserv
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AGENCOURT 8805197 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6196986 5', mRNA sequence.
BQ932168
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/rolone lib="Vector: pCWT-SPORT6 (Life Technologies); Site_1:
/note="Vector: pCWT-SPORT6 (Life Technologies); Site_1:
Directionally cloned using the following adaptors:
5. TCGACCACGCTCCG-3 and
5. GACTAGTTCTAGATCGCGAGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 Arccergecagracricaagacrecreceagecegecragecrereagecaggaagerr 120
                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 910)
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AGAA-GATCGTCCACA-GGGACATCAAGCCATCCAACCTGCTGGGGGATGATGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMI3606 row e column: 19
High quality sequence stop: 577.
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Pred. No. 3.4e-151;
0; Mismatches 31;
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/dev stage="adult, 70 yr"
/lab_host="DH10B"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6196986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                    864 CGTGAAGATCGCCGACTTTGGCGT 887
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                                                                                                                           840 GGTAAGCATCGGCAAGTAGGCGGT
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849; Conservative (
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                                                                               /dlone lib="NIH MGC 95"
//olone lib="NIH MGC 95"
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//olone lib="NIH MGC 95"
//octe="Organ: brain; Vector: pBluescriptk (modified pBluescript KS+); Site 1: BamH1; Site 2: Sall-XhoI (gtcgag); Oligo-dT primed using primer
s'-TTTTTTTTTTTTTTVW-3', Size-selected for average insert size 2: Sk band normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 880;
                                                                                                                                                                                                                                                                                                                                                               tch 49.0%; Score 742.4; DB 12; Length al Similarity 95.7%; Pred. No. 1.6e-153; 827; Conservative 0; Mismatches 31; Indels
                                            /tissue_type="hippocampus"
/lab_host="DH10B"
    'db_xref="taxon:9606"
'clone="IMAGE:4820238"
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Si
Matches 827;
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/tissue_type="forthcoarcinoma, cell line"
//lab host="DH10B (phage-resistant)"
//clone_lib="NIH_MGC_109"
//clone_lib="NIH_MGC_109"
//note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
//note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
//note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
//note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
//note="Organ: ovary; Vector: poTB7; Site_1: EcoRI; Site_2:
//note="Organ: ovary; Vector: poTB7; Site_2:
//note="Organ: ovary; Vector: poTB7; Site_2: Collifornia, Berkeley; using ZAP-oDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGCGTCACGTTGTACTGCTTTGTCTAT 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 723; DB 13;
Pred. No. 3.6e~149;
); Mismatches 15;
                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5804754"
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NH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                            GIGGCCATCTCAGATGCAGAGGACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGGTGAG
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TCCCTACAGGAGCGGCCAGCAGGAAGCTATCTGGAGGCGCAGGCTGGGCCTTATGCCACG
                                       GGGCCTGCCAGCCACATCTCCCCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCAC
                                                                                                               GIGGCCATCTCAGATGCAGAGGACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAG
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCX1302 row: 1 column: 04
High quality sequence stop: 733.
Location/Qualifiers
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602459214F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4581651 5'
CIGCTCCCAGCCCGGCCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGCCAGCA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/tissue_type="retinoblastoma"
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/db_xref="taxon:9606"
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972 bp mRNA linear EST 22-MAY-2003
BX459685 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CSODF003XD04 5-PRIME, mRNA sequence.
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/tissue_type="FETAL BRAIN"
/tissue_type="FETAL BRAIN"
/clone_lib="Home sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCWVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORY sites of the pCMVSPORT 6
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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      1404 GAGGGAAGAGCGATCCATGTC-TGCTCCAGGAAA--CCTACTGGTGAAAGAAGGG--TT
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF003DB02QP1.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8786.r
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/db_xref="taxon:9606"
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/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 16"
/note="Organ: eye; Vector: pOTB7; Site 1: Xho1; Site 2:
EcoR1; cDNA made by oligo-dT priming. Directionally
cloned into EcoR1/Xho1 sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH—MGC Library."
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0; Mismatches 34;
                                                                                                                                        Similarity 94.5%; 6; Conservative
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BX328136 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens EX328136 Homo sapiens PX328136 Homo sapiens HX328136 HOMO SAPIENS HAMA SEQUENCE.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-Length cDNA libraries and normalization
Unpublished (2001)
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/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/clone_lib="Homo cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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BP 191 91006 EVRY cedex - France
BF anil: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8786.r For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSOBAG049ZH12_CSO4704_1&cluster=8786.r.
cgi.bin/cluster.cgi?seq=CSOBAG049ZH12_CSO4704_1&cluster=8786.r.
Contact : Feng Liang Email : fliang@lffetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAG049ZH12_CSO4704_1.
Location/Qualifiers
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Pred. No. 8.1e-140;
0; Mismatches 19;
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/clone="CS0DK012YG22"
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gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITGGTGTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAAGTGCCCTGTGACAAGCCCTT
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44.1%; Score 668.6; DB 13;
Best Local Similarity 91.6%; Pred. No. 3.4e-137;
Matches 718; Conservative 0; Mismatches 65;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:5716218"
/tissue_type="whole brain"
/tissue_type="whole brain"
/dev stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="NIH BMAP FC0"
/note="Organ: brain; Vector: pXX-Asc; Site_1: EcoR I;
Site_2: Not 1; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCAGGAAAC--TACTGTGGAAGAGGTTTGTTGAAAGGGGCAAGAG-CCAAAGCTCC
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                314 ATTICATCCIGCCCTCCACAGGAAGAICAGAAIGAGCCCGIGGIGITICCTGAGGAGC
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                                                                                  CCGGCGTCCAGGAAGACGAGGCTGCATCC 1515
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/mol_type="mRNA"
/strain="C57BL/6"
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Location/Qualifiers
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4: /ogn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /ogn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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RESULT 2
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; Sequence 1, Application US/10135689
; Patent No. 6670162
; GENERAL INFORMATION:
; APPLICANF, WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
; FILE REFERENCE: CLO0090401V;
; CURRENT APPLICATION NUMBER: US/10/135,689
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR APPLICATION NUMBER: 09/729,995
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FRASLSEQ for Windows Version 4.0
; SEQ ID NO 1.
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Sequence 3, Application US/10135689
Patent No. 6670162
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE REFERENCE: THEREOF
FILE REFERENCE: CL0009040IV
CURRENT APPLICATION NUMBER: US/10/135,689
CURRENT FILING DATE: 2002-05-01
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CL000904
CURRENT APPLICATION NUMBER: US/09/729,995
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 09/729,995
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 4
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US-10-135-689-3
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; ORGANISM: Human
US-09-729-995-3
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; Sequence 3, Application US/09729995
; Patent No. 6426206
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS,
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; Patent No. 6500398
; GENERAL INFORMATION:
    APPLICANT: Janice Au-Young
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhamer
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                             Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      712 GTCATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCG 758
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APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                             DB 4;
                                                                                                                                                          Score 142.8; DB 4
Pred. No. 1.7e-27;
0; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3174 PORTER DRIVE
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                   Matches 203; Conservative
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                          ; LIBRARY: BRAINOT04
; CLONE: 926034
US-09-016-434-1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                        Similarity
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                             Query Match
Best Local 3
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                          ATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG
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Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
STREET: ALLO ALTO
STREET: CALIFORNIA
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COMPUTER READABLE FORM:
MEDIUM TYPER EPPOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SOFTWARE: WORD DATA:
APPLICATION NUMBER: US/09/016,434
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1008:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
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CITX: PALO ALTO
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                                                                                  Length 236;
                                                                                Score 99.4; DB 4; Length 2 Pred. No. 2.3e-16; 0; Mismatches 59; Indels
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Pred. No. 9.7e-14;
                                                                                                                                                                                                                                                                                                                                                881 ITGGCGTCAGCAACCAGTTTGAGGGGAACGACGCTC
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APPLICATION NUMBER: US/08/913,050A
FILING DATE: 0.528P-1997
FILING DATE: 0.528P-1997
FILING DATE: 1.6-MR-1995
FILING DATE: 1.6-MR-1995
FILING DATE: 1.6-MR-1995
FILING DATE: 1.6-MR-1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: BROWDY AND NEIMARK, P.L.L.C. 419 7th Street N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08913050A
Patent No. 5827726
GENERAL INFORMATION:
APPLICANT: NEZU, Jun-ichi
                                                                                  6.6%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                Query Match 6.6
Best Local Similarity 71.8
Matches 155; Conservative
                 LIBRARY: BRAINOT03;
CLONE: 531037
US-09-016-434-809
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Best Local Similarity
     IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGACATCAAGCCATCCAACCTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCGAC 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582
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                                                                       Greangaaggaarrcaacracreaegaggrracegcacaaaaargrcarccagcregere
                                                                                                                                                                                                                                            343 GATGTGTTATACAACGAAGAAGCAGAAATGTATATGGTGATGGAGTACTGCGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                        403 gecarecadaaargeriddacagegreecegagaagegrrireecagreecaggeeeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             760 CTCTACCTGCGGGACGTCATCCTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 GGGTACTICTGTCAGCTGATTGACGCCCTGGAGTACCTGCATAGCCAGGGCATTGTGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 523 AAGGACATCAAGCCGGGGAACCTGCTCCTCACCGCTGGCACCTCAAAATCTCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          643 Gerrecegerrinecagecececesão -- Arreceacesecresacacarerreres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       760 CCCTTCGAAGGGGACAACATCTACAAGTTGTTTGAGAACATCGGGAAGGGGAGCTACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1114 TITCCIGAGGAGCCAGAAAICAGCGAGGAGCICAAGGACCIGAICCIGAAGAIGTIAGAC
586 GIGIACCAGGAGAIIGCCAICCIGAAGAAGCIGGACCACGIGAAIGIGGGICAAACIGAIC
                                                                                                                                                                                                                                                                                                                        700 AGAAAGGGCCCCTCATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGC
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Batent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
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GIGIACCAGGAGATIGCCATCCTGAAGAAGCTGGACCACGTGAATGTGTCAAACTGATC 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          646 GAGGTCCTGGATGACCCAGCTGAGGACAACCTCTATTTGGTGTTTGA-
                                                                                                                                                                                                                                                                                                                                           GENERAL INPORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 87; DB 2; Le
ilarity 50.0%; Pred. No. 7.7e-13;
Conservative 0; Mismatches 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: INCYTE PHARMACEUTICALS, INC 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING DATE: Filed Herewith
APPLICATION NUMBER:
FILING DATE:
ATTOMATE APPLICATION NUMBER:
FILING DATE:
ATTOMATE APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.,
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0150 US
TELEPHONE: 415-985-0555
                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08749902
Patent No. 5985635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1466 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus
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Best Local Similarity
Matches 331; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
                                                                             AA 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 GIGAAGAAGGAAATICAACTACTGAGGAGGTTACGGCACAAAAATGTCATCCAGCTGGTG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               669 BLOCICO----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGTGTTATACAACGAAGAAGCAGAAAATGTATATGGTGATGGAGTACTGCGTGTGT 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGACATCAAGCCGGGGAACCTGCTGCTCACCACCGGTGGCACCCTCAAAATCTCCGGAC 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTACTTCTGTCAGCTGATTGACGGCCTGGAGTACCTGCATAGCCAGGGCATTGTGCAC 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          700 TICAAGGIGGACAICIGGICGGCIGGGICACCICIACAACAICACCACGGGICIGIAC 759
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Pred. No. 9.7e-14;
0; Mismatches 306; Indels 21
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                                                                                                                                                                                                                                                                                                                                                                           PA-0002 US
CURRENT APPLICATION DATA: US/09/016,434
                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUYBER: PA-000
TELECOMMUNICATION INFORMATION:
TELEPRAM: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1146:
SEQUENCE CHARACTERISTICS:
LENGTH: 1302 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 6.0%;
al Similarity 50.6%;
335; Conservative
                                                                                      HEREWITH
                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                         APPLICATION NUMBER:
FILING DATE: HEREWI
CLASSIFICATION:
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US-09-016-434-1146
                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343
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Best Local
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APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
FILE REPERENCE: RTS-0035
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CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 47
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729 TGACAAGCCTTCTCGGAGGAGCAAGCTCGCTGTGCGGGACGTCATCCTGGGGCCT
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                                                                                                                                            9 9 TTTGGCGTCAGCAACCAGTTTGAGGGGAACGACGCTCAGCTGTCCAGCACGCC----G
                                                                                                                                                                                                                                   882 CTGGGCGTGGCCGAGGCACTGCACCGTTCGCNGCGGACGACACCTCCGGACCAGCCAG
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APPLICANT: MAIBULIT, KOZO
APPLICANT: ONO, YOSHITAKA
APPLICANT: ONO, YOSHITAKA
TITLE ONO, YOSHITAKA
TITLE OF INVENTION: MODIFIED PROTEIN DERIVED FROM PROTEIN KINASE N
FILE REPERENCE: 016897/0844
CURRENT FILING DATE: 1996-07-24
CURRENT FILING DATE: 1996-07-24
PRIOR APPLICATION NUMBER: UP 7-262552
PRIOR APPLICATION NUMBER: UP 7-344606
PRIOR APPLICATION NUMBER: UP 8-080549
PRIOR FILING DATE: 1996-03-08
PRIOR PLILING DATE: 1996-03-08
PRIOR RILING DATE: 1996-04-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VORTER: 1996-04-11
SEQ ID NOS: 6
SOFTWARE: PATENTIN VEY: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08685852
Patent No. 6660837
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , NAME/KEY: CDS
; LOCATION: (37)..(2862)
US-08-685-852-1
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-----TGGCCGGGCCGTGGAC 1083
            TICATGGCCCCCGAGGCCATTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGAT 1005
                                                                                                                                    1006 GTAIGGGCCACTGGCGTCACGTIGIACTGCTTTGTCTATGGGAAGTGCCCATTCATCGAC 1065
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                                                                                                                                                                                                                                                                                                                         1144 CAGGACCACGAGCGCCTCTTCGAGCTCCTCATGGAAGAGGATCCGCTTCCC-----G
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Pred. No. 6.7e-12;
0; Mismatches 226; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhamer
IITLE OF INVENTION: COMPOSITION FO
IITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1186 ACGAGAATTGGGGTG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1258 CAGAGGCTTGGTGGG 1272
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STRANDEDNESS: single
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CALIFORNIA
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Best Local Similarity
Matches 254; Conserv
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US-09-023-655-1004
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1198 GCACGCTCAGCCCCGAGGCCAAGTCCCTGCTTGCTGGGCTGCTTAAGAAGGACCCCCAAG 1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCCCGTCATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGAGGAAGCTCGCCTCTAC 765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S. Bragland, James M. FITLE OF INVENTION: CANCER VACCINE NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN NCHORE: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <unhaperature compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible compatible com
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NAME: MODACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09167322
Patent No. 6365151
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
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STRANDEDNESS: single
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Best Local 3
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271 TACTCCTTCCAGGAC ---GAGGAGGACATGTTCATGGTCGTGGACCTGCTACTGGGCGGG 327
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APPLICANT: Meyers, Rachel
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: 35800/209996
CURRENT APPLICATION NUMBER: US/09/799,875
CURRENT FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 6/182,059
PRIOR PILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 6/182,059
PRIOR PILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/659,287
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Pred. No. 1e-11;
0; Mismatches 192; Indels 6
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6638721
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224; Conservative C
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US-09-799-875-13
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ORGANISM: Homo sapiens
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US-09-799-875-13
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Williamson, Mark
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
FILE OF INVENTION: Therefor
CURRENT APPLICATION NUMBER: US/09/799,875
CURRENT APPLICATION NUMBER: 60/182,059
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-09-11
PRIOR FILING DATE: 2000-09-12
NUMBER: OF SEALCH OF WAIGHTER 109/659,287
PRIOR FILING DATE: 2000-09-12
NUMBER: OF SEALCH OF WAIGHTER 109/659,287
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Pred. No. 8.7e-12;
0; Mismatches 192; Indels
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Best Local Similarity 53.1%;
Matches 224; Conservative 0
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CORGANISM: Homo sapiens
US-09-799-875-15
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Search completed: July 25, 2004, 11:37:16 Job time : 147 secs

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The invention relates to an isolated peptide designated human kinase

(HK), that has homology to members of the calcium/calmodulin-dependent

protein kinase kinase subfamily. The mechanism of action of the protein

of the invention is that of a kinase modulator. The human kinase of the

creating a disease or condition mediated by the human kinase. HK is also

treating a disease or condition mediated by the human kinase. HK is also

useful to provide a target for diagnosing a disease or predisposition to

disease mediated by HK, and is also useful in pharmacogenic analysis. HK

creating to treating a disorder characterised by absence of

inappropriate or unwanted expression of HK, also as an immunogen to raise

antibodies by administering HK to a mammalian organism e.g. rat, rabbit

or mouse. Nucleic acids of the invention are useful as hybridisation

probes for mRNA, transcript/conNA and genomic DNA. Recombinant host cells

expressing a native HK are useful for assaying compounds that stimmlate

cor inhibit HK function. Nucleic acids of the invention are also useful

for producing transgenic animals. Experimental data indicates that kinase

cor inhibit the gressent invention are expressed in humans in the eye

fretinoblastomas) and brain. The current sequence represents cDNA

cording the human kinase of the invention
a disease or predisposition to the disease mediated by the peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2190 BP; 457 A; 655 C; 708 G; 370 T; 0 U; 0 Other;
                                                                Claim 4b; Fig 1; 89pp; English
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Op	1553 AACCCGTTT	ဥ္က
δλ	1441 CTGGTGAAA	TGAAAGAAGGTTTGGTGAAGGGGGAAAAGCCCAGAGGTCCCCGGCGTCCAGGAA 1500
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RESU AAD3 ID	ULT 2 30566 AAD30566 standard;	CDNA, 1937 BP.
AC A		
\$E\$	21-MAY-2002 (first	: entry)
E X	Human kinase polyp	eptide (PKIN-19) cDNA.
KW	Human; kinase polypept	<pre>>eptide; PKIN-19; gene therapy; Addison's disease;</pre>

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leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertenaion; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antinfiammatory; hepatocropic; New human kinase polypeptide, useful in diagnosis, prevention and treatment of cancer, immune disorder, growth and developmental disorder, cardiovascular disorder and lipid disorder. Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia NK, Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR; Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Dii Yao MG, Blliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL; /product= "Human PKIN-19" Claim 5; Page 193-194; 196pp; English. Location/Qualifiers hypotensive; anti-HIV; enzyme; ss. 2000US-0220038P. 2000US-0222112P. 2000US-0222831P. 20-JUL-2001; 2001WO-US023092 2000US-0224729P GENOMICS INC 65. .1582 /*tag= a WPI; 2002-206083/26 (THOR/) THORNTON M. P-PSDB; AAE19161. (INCY-) INCYTE WO200208399-A2 21-JUL-2000; 2 28-JUL-2000; 2 04-AUG-2000; 2 11-AUG-2000; Homo sapiens 31-JAN-2002

The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's disease, rheumatoid arthritis, a growth and developmental disorder (e.g. bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarcinon), and a liphid disorder (e.g., fatty liver, cholestasis, Gaucher's disease, Niemann-Pick's disease, PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting cell ferences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridisation to probes for mapping naturally occurring genomic sequences. PKIN is useful cell contern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme conterns or conterns partients to detect altered PKIN expression. The sequence is human PKIN-19 cDNA

DB 6; Length 1937; Sequence 1937 BP; 425 A; 567 C; 603 G; 342 T; 0 U; 0 Other; Score 1510.2; Pred. No. 0; 0; Mismatches 99.7%; Query Match Best Local Similarity 99.8 Matches 1512; Conservative

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GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCCGTTCATCGACGATTTCATCCTGGCC 1144 180 240 480 720 780 300 360 420 304 364 424 484 540 600 999 724 784 844 840 960 604 904 964 125 GCAGCCATCGATGTGACTCACTTGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC GGTGTGGACCCCCCCACACGGGCCAGAGCTGCCTCTGTGATCCCTGGCATACTTCAAGA CTGCTCCCAGCCCGGCCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGCCAGCA 365 CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC ccaecteaegacaactertriegretrieaccrecteagaaagegeccercargaa GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCCAGAGCCTACTAGAAAC GGTGTGGACCCCCACCACGGGCCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC CIGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAAC GAGGGAACGCTCAGCTGTCCAGCACGCGGGAACCCCAGCATTCATGGCCCCCGAG CTGCTCCCAGCCCGGCCTTCTCAGCCAGGAAGCTTTCCCTACAGGAGCCGAGCA GACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAGATTGGCAAAGGGTGCCTACGGT GTGGTGAGGCTGGCCTACAACGAAGTGAAGACAGACACTATGCAATGAAAGTCCTTTCC GIGGIGAGGCIGGCCIACAACGAAGIGAAGACAGACACIAIGCAAIGAAAGICCIIIICC AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGTCCCAG AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCTCCCCGGAGAGGGCCCAG GCTGCCCAGGGAGCACCAGCCAAGCAGCTGCTGCCCTGGAGCGGGTGTACCAGGAGATT GCTGCCCAGGAGGACCAGCCAAGCAGCTGCTGCCCCTGGAGCGGGTGTACCAGGAGATT CCAGCTGAGGACAACCTCTATTTGGTGTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAA GTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATC CTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAAC CIGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT CTGCTCCTGGGGGATGATGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT GAGGGGAACGACGCTCAGCTGTCCAGCACGCGGGAACCCCAGCATTCATGGCCCCCGAG GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCATCTGGCC GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC GACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT 185 181 545 121 245 241 305 301 361 425 485 481 541 605 601 665 725 721 785 845 841 905 901 965 1021 1085 61 421 661 781 196 d à 셤 ð g ð g à g δ qq ò d à g ò qq ò 요 ∂ d ò g δ 셤 ò d δ g à g à g à d

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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-600 ABZ12106) or their mature protein coding portion, active domain coding praction, active domain coding praction, active domain coding praction or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABE6890-ABE68949) are useful as molecular weight markers as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellopidisorders (cancer), neurodegenerative diseases (Parkinson's proliferative disorders (cancer), neurodegenerative diseases (Parkinson's diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                   CTCCACAGGAAGATCAAGAATGAAGCCCGTGGTTTTCCTGAGGAGCCAGAAATCAGCGAG
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 CTCCACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCAGAAATCAGCGAG
                                                                    GAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTGGGGTG
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Yamazaki V, Chen R, Wang Z, Ghosh M;
FD, Drmanac RT;
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Tang Y, Ma Y, Yamazak
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T, Wang J,
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18-OCT-2001;
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10-SEP-2001;
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27-SEP-2001;
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                    GCTGCCCAGGGAGGACCAGCCAAGCAGCTGCCCCTGGAGCGGGTGTACCAGGAGTT
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                              Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Gusev V, Ji W, Gorman L, Miller CE, Kekuda Gangolli E, Vernet CAM, Guo X, Tchernev V; Casman SJ, Malyankar UM, Gerlach V, Liu Y, Catterton E, Burgess C, Leite M, Zhong H, A
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Best Local Similarity 99.6%;
Matches 1509; Conservative
                                                                                                                             Lepley DM, Rieger DK,
CURAGEN CORP
                                                                                                                                                                        WPI; 2002-723332/78.
                                                                                                                                                                                                                                                                                                                             Claim 13; Page 139;
                                                                                                                                                                                        P-PSDB; ABU65068
                                Padigaru M, Sp.
Zerhusen BD, G.
Patturajan M, G.
Fernandes ER,
                                                                                                               Spaderna SK,
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disorders (e.g. atherosclerosis), disorders of bone metabolism (e.g. osteoporosis) and haematopoietic disorders (e.g. arthritis). The present

(first entry)

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Human cDNA 16002 encoding a novel kinase
  15-JUL-2002
                                   Meyers RA,
ABK49563;
                  Key
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Human; ss; gene; 16002; kinase; cellular proliferative disorder; cancer; carcinoma; tumour; adenocarcinoma; haematopoietic neoplastic disorder; leukaemia; lymphoma; brain disorder; cerebral ischaemia; infection; meningitis; brain abscess; acquire immunodeficiency syndrome; obesity; AIDS-related myopathy; prion disease; Alzheimer's disease; diabetes; Parkinson's disease; Huntington's disease; motor neurone disease; metabolic disorder; anorexia nervosa; pain; inflammation; ischaemia; irritable bowel syndrome; heart disorder; motor accordial infarction; blood vessel disorder; atherosclerosis; bone metabolism disorder; osteoporosis; haematopoietic disorder; arthritis. /product= "Kinase 16002" /note= "This coding sequence (minus the stop codon) is specifically claimed in claim 1" iocation/Qualifiers Silos-Santiago I; (MILL-) MILLENNIUM PHARM INC. 01-SEP-2000; 2000US-022929P 03-AUG-2001; 2001WO-US024601 198. .1883 ಹ /*tag= WPI; 2002-351781/38. P-PSDB; AAU79458. WO200220800-A2 Homo sapiens.

The invention relates to an isolated human kinase polypeptide encoded by the DNAs designated 16658, 14223 and 16002 included are a host cell comprision to be monologues and allelic variants. Also included are a host cell comprising the monologues and allelic variants. Also included are a host cell comprising the novel kinase, and recovering the protein, detectively binds to the novel kinase, and recovering the protein, detecting the presence of the DNA in a sample comprising contacting the sample with a compound which selectively hybridises to the DNA and determining whether the compound has bound and identifying compounds which bind to and/or modulate the protein comprising contacting the protein with a test compound and determining whether the compound has bound to and/or modulated the function of the protein (the modulators may be a samall molecule, a peptide, a phosphopeptide, an antibody or a fragment of the full length protein). The nucleic acids, proteins, identified modulators and antibodies are useful in the diagnosis, monitoring and treatment of a wide range of diseases and disorders (many examples of which are listed in the protein protein and brasely and promoters advantaged to the listed in the diagnosis. of the lung and breast, carcinomas, tumours, adenocarcinomas, haematopoietic neoplastic disorders e.g. leukaemias and lymphomas), brain and nerve tissue disorders (e.g. cerebral ischaemia, infections such as meningitis, brain abscess, acquirted immundeficiency syndrome (AIDS)-related myopathy, prion diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease and motor neurone disease) metabolic disorders (e.g obesity, anorexia nervosa and diabetes) pain disorders (e.g. associated with infection, inflammation ischaemia, irritable bowel syndrome), heart disorders (e.g. myocardial infarction), blood vessel New human transferase protein for diagnosing and treating disorders e.g. cancer, Alzheimer's disease, anorexia, diabetes and to identify Claim 1; Fig 16; 143pp; English. modulators for therapeutic use.

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                                                                                               Length 2711;
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                                                               C; 848 G; 508 T; 0 U; 11 Other;
                                                                                                                              Indels
                                                                                               DB 6;
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                                                                                               Score 1490.6;
                                                                                                              Pred. No. 0;
0; Mismatches
                               sequence encodes novel human kinase 16002
                                                               Sequence 2711 BP; 592 A; 752
                                                                                             98.4%;
ilarity 99.4%;
Conservative
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AASO6701-AASO6757 encode for novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides or serine/threonine kinase (PTK and STK) families. The polynucleotides or serine/threonine kinase (PTK and STK) families. The polynucleotides or serine/threonine kinase and the polypeptides may be used in the prevention, diagnosis and treatment of disease associated with the amorphy propriate kinase expression. For example, they may be used to treat cancers (especially cancers of the amount of disease associated with the cancers of actions of the amount of disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility).

Additionally, polynucleotides encoding protein kinases may be used as antigens in the production of antibodies against the protein kinase sand in assays to identify modulators of protein kinase expression and activity
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                          encoding human kinase polypeptides, useful for preventing 1/or treating e.g. cancer, immune, cardiovascular and
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1542;
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                                             diagnosing and/or treating e.g. cancer, immune, cardion
neuronal-associated diseases, and microbial infections.
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                                                                                                                                                 metabolic disorder; immune related disease; neurological disorder;
neurodegenerative disorder; inflammatory disorder; infectious disease;
reproductive disorder; gene therapy; ss.
                                                                                                                             CTCCACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCCAGAAATCAGCGAG
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                                                                       GTCAAACTGATGGAGGTCCTGGATGACCCAGCTGAGGACAACCTCTATTTGG
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The invention relates to novel human kinase proteins (PKIN) and nucleic acid molecules encoding them. PKIN is useful for identifying compounds that modulates its activity. PKIN cDNA is useful for assessing toxicity of a test compound. PKIN and its cDNA are useful for diagnosis, prevention and treatment of immune disorders such as acquired immune prevention and treatment of immune disorders such as acquired immune distress syndrome (AIDS), Addison's disease, anaemia, autorimmune thyroiditis, multiple sclerosis, asthma, asteoasthrifis, osteoarthrifis, osteoarthrifis, osteoarthrifis, orderative colitis and diabetes mellitus; growth and developmental disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, burstits, cirrhosis, cancers such as adenocarcinoma and leukaemia, cardiovascular diseases such as adenocarcinoma and leukaemia, cardiovascular diseases such as myocardial infarction and hypertension, and lipid disorders such as myocardial infarction and hypertension, and lipid disorders such as grounders and regulatory elements, for creating knock in or knock out in humanised animals or transgenic animals to model human disease and for somatic or germline gene therapy for treating the above
             Human kinase; PKIN-2; therapy; immune disorder; Addison's disease; AIDS; acquired immune deficiency syndrome; growth and developmental disorder; arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma;
                                                                   leukaemia; cardiovascular disease; myocardial infarction; hypertension; lipid disorder; cancer; fatty liver; cholestasis; transgenic animal; gene therapy; antiallergic; antiasthmatic; antithyroid; dermatological; antidiabetic; nephrotophic; antiulcer; antiarthritic; antirheumatic; antipsoriatic; neuroprotective; cytostatic; hepatotrophic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human kinase proteins (PKIN) useful for diagnosing, treating, preventing immune disorders, cardiovascular diseases and disorders affecting growth and development associated with abnormal expression
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Pred, No. 0;
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0; Mismatches
                                                                                                                                                                  vasotropic; antianginal; anorectic; ss
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                                                                                                                                                                                                                                           Location/Qualifiers
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P, Khan FA;
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14-JAN-2000; 2000US-0176107P-
28-JAN-2000; 2000US-01731P-
28-JAN-2000; 2000US-01735P-
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Best Local Similarity 97.9%;
Matches 1509; Conservative
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Tao MG, Lal
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ATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG

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AAD08635 standard; cDNA; 3501

Human kinase (PKIN) -2 cDNA

(first entry)

04-SEP-2001

AAD08635;

RESULT 7
AADO8635
ID AADO
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AC AADO
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DT 04-S
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Qy 1114 TTTCCTGAGGAGCCAGAATCAGCGAGGACTCAAGGACTGATCCTGAAGATGTTAGAC 1173 Db 1202 TTTCCTGAGGAGCCAGAATCAGCGAGGACTCAAGGACTTAGACTTAGACTTAGACTTAGACTTAGACTTAGACTCAAGATTAGACTCAAGAATCAGATCAAGAATCAGACTCAAGAATCAGACACAAGAATCAGACACAAGAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAAATCAGAAATCAGAAAAAAAA	ABX97034 ID ABX97034 ABX97034 ABX97034; ABX97034; XX ABX97034; XX ABX97034; XX ABX97034; XX CAMAY-2003 (first entry) XX DAWAY-2003 (first entry) XX NOVX; Cytostatic; Cardiant; antiarteriosclerotic; antiasthmatic; cancer; XX NOVX; Cytostatic; Cardiant; bronchial asthma; gene therapy; vaccine; XX XX Home sapiens. XX XX WC CO0272757-A2. XX WC CO0272757-A2. XX WC CO0372757-A2. XX C C C C C C C C C C C C C C C C C C
и н й ц й н и н и н и н и	454 AGACACTATGCAATGAAAGTCCTTTCCAAAAGAAGTTACTGAAGCAGTTTCCA 614 545 AGACACTATGCAATGAAAGTCCTTTCCAAAAAGAAGTTACTGAAGCAGTTTCCA 604 546 AGACACTATGCAATGAAAGTCCTTTCCAAAAAGAAGTTACTGAACGACTATGCGTTTCCA 604 547 GATCGCCCTCCCCCCGAGAGGTTCCCAAAGAAGTTACTGAACAACCAAACAAGTTCTCA 664 548 GATCGCCTCCCCCCGAGAAGGTTCCCAAGGAACCTCCAACCAA

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Claim 13; Page 138; 1103pp; English.
                                                                                                                                     2001US-0293027F.
2001US-029303P.
2001US-029310P.
2001US-0304354P.
2001US-031299P.
2001US-0312903P.
                          2001US-0280802P
2001US-0280802P
2001US-0280900P
2001US-0281575P
2001US-02817424P
2001US-02881367P
2001US-0288342P
2001US-0288528P
2001US-0288528P
2001US-029190P
2001US-0291190P
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2001US-0325430P.
2001US-0325681P.
2001US-0330380P.
2001US-0335301P.
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2001US-0294899P.
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2001US-0333272P.
2001US-0332094P.
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2001US-0338092P
2001US-0337185P
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P-PSDB; ABU65067.
                                         02-APR-2001; 2
04-APR-2001; 2
30-APR-2001; 2
30-APR-2001; 2
02-MAY-2001; 2
03-MAY-2001; 2
15-MAY-2001; 2
16-MAY-2001; 2
                                                                                                                                              19-JUN-2001;
19-JUN-2001;
10-JUL-2001;
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16-AUG-2001;
10-SEP-2001;
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27-SEP-2001;
27-SEP-2001;
18-OCT-2001;
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31-MAY-2001;
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21-NOV-2001;
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14-NOV-2001;
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Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
Lepley DM, Rieger DK;

NOVX polypeptides and polynucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial

cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABX97008-ABX97185 are cDNA fragments amplified and isolated by the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-ABX97088-ABX97185 encode the NOVX proteins described in ABX97186-ABX97088-ABX97185. This invention describes novel human NOVX polypeptides which have

120 420 439 480 499 540 009 619 099 139 180 199 240 259 300 319 360 619 720 780 900 916 916 736 796 856 09 79 80 GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC 140 GGTGTGGACCCCCCACCACGGGCCAGAGCTCTCTGTGATCCCTGGCAGTACTTCAAGA CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG GTGGTGAGGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCCTTTCC 440 GTGGTGAGGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCCTTTCC 500 AAAAAGGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGTCCCAG GCTGCCCAGGGAGGACCAGCCAAGCAGCTGCCCCTGGAGCGGGGTT 20 ATGGAGGGGGGCTCCTGCTGCTGCCAGGATCCTCGGGCAGGCTGGTAGAACGGGTG GCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCCTACTAGAAAC 320 CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG GACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT 380 GACTGCGTGCAGCTGAACCAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACGGT AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCCGAGAGGGTCCCAG GCTGCCCAGGGAGGACCAGCCAAGCAGCTGCTGCCCCTGGAGCGGGTGTACCAGGAGATT 601 GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC 620 GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTACTGGATGAC CCAGCTGAGGACAACCTCTATT---TGCCCCGCATCCTTCTCCATAGGCCCGTCATGGAA GTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATC GTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATC CIGGGCCTCGAGTACGTGCCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAAC GAGGGGAACGACGCTCAGCTGTCCAGCACGGGGAACCCCAGCATTCATGGCCCCCGAG 917 GAGGGGAACGACGCTCAGCTGTCCAGCACGGCGGGAACCCCAGCATTCATGGCCCCGAG 1 ATGGAGGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG CTGCTCCCAGCCCGGCCTTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGGCCAGCA CCAGCTGAGGACAACCTCTATTTGGTGTTTGACCTCCTGAGAAAGGGGCCCGTCATGGAA CTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGGACATCAAGCCATCCAAC 857 CIGCTCCTGGGGGAIGAIGGGCACGIGAAGAICGCCGACTTTGGCGICAACAACAGTTT GGTGTGGACCCCCCACCACGGGCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA CTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCGACTTTTGGCGTCAGCAACCAGTTT Gaps DB 6; Length 1547; 9 Sequence 1547 BP; 352 A; 441 C; 474 G; 280 T; 0 U; 0 Other; 17; Indels Score 1455.8; Pred. No. 0; 0; Mismatches Query Match Best Local Similarity 98.5%; Matches 1492; Conservative 260 089 737 (301 361 661 721 797 841 61 121 181 241 421 481 541 781 901 196 XX Db d g g ð g q à Ωp Db ò g g d dd ò d δ g δ q ð ò ð ò $\dot{\delta}$ 8 ò ò ò à à g

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This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive
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   2001US-0277239P.
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2001US-0277321P.
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2001US-0277331P.
2001US-0278894P.
2001US-027899P.
2001US-027893P.
2001US-0279344P.
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29-MAR-2001;
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GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAG---TTGGATGTATGGGCCACTGGC
                                                                   CTCCACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCAGAAATCAGCGAG
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                                                                                                                 GAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTGGGGTG
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                        GICACGITGIACTGCITIGICIAIGGGAAGIGCCCAIICAICGACGAITICAICCIGGCC
                                     1034 GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCATCCTGGCC
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09-MAR-2001; 2001US-0274849P.
12-MAR-2001; 2001US-027523F.
13-MAR-2001; 2001US-0275579P.
13-MAR-2001; 2001US-0275579P.
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activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atheoscalerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABX97108-ABX97185 are cDNA fragments amplified and isolated by the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-ABX97008-ABX97185 encode the NOVX proteins described in ABX05041-ABU65218
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Best Local Similarity 92.6%;
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đ	bb 892 TGTGACAAGCCCTTCTCGGAGGAAGCTCGCCTCTACCTGCGGGACGTACCTGGGG	
ð	Qy 787 CICGAGIACITGCACIGCCAGAAGAICGICCACAGGGACAICAAGCCAICCAACCIGCT	ω υ –
d d	0	ATCCAACCTGCTC 1011
8 8	QY 847 CTGGGGGATGAFGACGTGAAGATCGCCGACTTTGGCCTCAGCAACCAGTTTGAGGG Db 1012 CTGGGGGATGATGACGCACGTGAAGATCGCCGACTTTGGCCGTCAGCAACCAGTTTGAGGGG	CCAGTTTGAGGGG 906
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Ø ä	QY 1147 AAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTGGGGTGCCAGAC	TGGGGTGCCAGAC 1206 TGGGGTGCCAGAC 1371
õ	1207 ATCAAG	12
ď	Db 1372 ATCAAGTTGCACCCTTGGGTGACCAAGAACGGGGGGGGGG	
8 G	Qy 1267 CACTGCAGCGTGGTGAGCTGACAGGGGGGGGGGTTAAGAACTCAGTCAG	CAGGCTCATCCC 1326
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ជ	Db 1492 Actiggaccacggigarictiggigaagiccatgctgaggaaggatcctttgggaagcccg	Н
8	Qy 1387 TITGAGCCCCAGGCACGGAGGAAGAGCGATCCATGTCTGCTCCA	CCAGGAAACCTACTGGTG 1446
Ωį	1552	AAACCTACTGGTG 1611
8	OY 1447 AAAGAAGGTITGGTGAAGGGGGCAAGAGCCCAAGAGCTCCCGGGGTCCAGGAAGACGAG	150
đ	1612	ccaecaacaccae 1671
8	Oy 1507 GCTGCATCC 1515	
ă	1672	
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¥ II I		
X ¥	XX AC ADB53308;	
253	XX DT 04-DEC-2003 (first entry)	
2 2 2	Primary rat hepatocyte	SEQ ID NO:3850.
222	KW toxic effect; gene expression profile; hepatotoxicity; KW toxicity marker; toxicity progression; drug screening; KW primary rat hepatocyte toxicity modelling; dene; ds.	diagnostic marker;
S &	Rattus norvegicus.	
Z E	WO2003065993-A2.	

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                                                                                                                                                                                                                                                                                                                                                                      Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox mean values.
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                                                        2002US-0353171P.
2002US-0363534P.
2002US-0370248P.
2002US-0371134P.
2002US-0371135P.
2002US-0371150P.
2002US-0373601P.
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2002US-0378653P.
2002US-0378665P.
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11-APR-2002;
19-APR-2002;
22-APR-2002;
22-APR-2002;
09-MAY-2002;
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                                           CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACCACGTGGCCATCTCAGATGCAGAG
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Pred. No. 3.8e-298;
0; Mismatches 174; Indels 0;
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Best Local Similarity 88.5%;
Matches 1341; Conservative
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                                                                        AACCCATTIGAGCCCCAAGCACGCAGGAAGAACTTGTTGTTGTCTGCGCCAGGAAACTTA 1546
                                                                                                        CTGGTGAAAGAAGGGTTTTGGTGAAGGGGGCAAGAGCCCAGAGGCTCCCCGGCGTCCAGGAA 1500
                                                                                                                     detecting CSIGP related sequences or allelic variants. Recombinant CSIGP can be produced in host cells by transforming them with genetically engineered vectors. Agonists or antagonists can be used in the treatment of cell proliferative and inflammatory disorders associated with decreased or increased CSIGP expression. CSIGP is used in the diagnosis, prevention and treatment of cell proliferative disorders like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders like htbs, Addison's disease, multiple sclerosis, etc.
                                                                                                                                                                                                                                                                                                                                    Cell signalling protein-2; CSIGP-2; cell proliferation; arteriosclerosis; inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS; Addison's disease; multiple sclerosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a cDNA obtained from Incyte clone 640521 of BSENTWOTO 31 library. It encodes cell signalling protein. 2 (CSIGF-2). It is expressed in reproductive, nervous and developmental tissues. Fragments of CSIGP encoding nucleic acid can be used as hybridisation probe for
           ATCCCCAGCTGGACCACGGTGATCCTGGTGAAGTCCATGCTGAGGGAAGCGTTCCTTTGGG
                                                          AACCCGTTTGAGCCCCAGGCACGGAAGGGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTA
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241. .1860
/*tag= a /product= "Cell Signalling Protein-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cell signaling proteins useful for, e.g. proliferative and inflammatory disorders.
                                                                                                                                                                                                                                                                                                              Human cell signalling protein-2 encoding cDNA
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                                                       Score 660.2; DB 3;
Pred. No. 2.3e-154;
0; Mismatches 353;
Sequence 2545 BP; 542 A; 737 C; 760 G;
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Best Local Similarity 71.3%;
Matches 885; Conservative
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                                                                                                                                        the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to newly discovered cancer markers associated with
1578 CACGAGGCATGGGGCGGAGCCGTTGCCGTCGGAGGATGAGAACTGCACGCTGGTCGAAGT
                                                                                    GGAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAAGAAGGGTTTGGTGAAGG
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M, Glatt K, Zhao X,
                                                                                                                                                                                                                                                                                                                                           Prostate; cancer; cytostatic; gene therapy; marker;
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12-DEC-2001; 2001US-0341146FP.
05-MAR-2002; 2002US-0362158P.
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Sequence 4942 BP; 1169 A; 1294 C; 1356 G; 1122
                                               Score 651.2; DB
Pred. No. 5e-152;
                                          tch 43.0%;
al Similarity 71.3%;
873; Conservative
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                                                                                                                     Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-
                                                                       GGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTCGAGGGC---AGCCGGCG
                                                                                              GGAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAAGAAGAAGGGTTTGGTGAAGG
GACAGAGGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTGGACCACGGTGATCCT
                      GACTGAAGAGGGTCGAGAACTCAGTCAAACACATTCCCAGCTTGGCAACCGTGATCCT
                                               GGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAACCCGTTTGAGCCCCCAGGCACGGAG
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diagnosing and treating prostate cancer in mammals. The prostate cancer-
associated genes are useful for diagnosing or treating prostate cancer,
as well as for identifying modulators of prostate cancer or agents that
inhibit prostate cancer. The nucleic acid sequences are particularly
useful in gene therapy, as a vaccine or in antisense applications.
ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
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71.5%; Pred. No. 3.9e-152;
iive 0; Mismatches 345;
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associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived

from the tissues of various organisms such as humans or other (e.g. mice, sheep and dogs). The methods of the invention are

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Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous tipluries, peripheral nervous injuries, and inseases, such as Alzheimer's, Parkinson's disease, Autington's disease, amyotrophic aleren's cleavesis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity chemotactic/chemokinetic activity, haemostatic activity, chemotactic/chemokinetic activity, haemostatic and thrombolypic activity, arthritis and inflammation, leukaemias and c. N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00598042.
19-JUL-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-006930344.
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Wang Z, Wehrman T,
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	1253 CICCACAGGAAGATCAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCAGAATCAGCGAG 1141 GAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTGGGGTG 1313 GAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTGGGGTG 1201 CCAGACATCAAGAATTGCACCTTTGGGTGACAAGAACGGGGGGGG	1373 CAGACATCAAGTTGCACCTTGGGTGACGAGGAGGAGGAGGAGGAGCCCTTCGGAG 1261 GAGGAGCACTGCACCCTTGGGTGACACGGGGAGGAGGAGCCCCTTCGGAG 1433 GAGGAGCACTGCAGCGTGGAGGAGGTGACAGGGGGAGGAGGTTAAGAACTCAGTCAG	1381 AACCCGTTTGAGCCCCAGGCAGGGAACAGCGATCCATGTCTGCTCCAGGAAACCTA 	RESULT 2 AX406674 LOCUS DEFINITION Sequence 1 from Patent W00224920. ACCESSION AX406674 AX406674 AX406674 AX406674 AX406674 AX406674.1 GI:21439624 KENWORDS GRANISM Homo sapiens (human) ORGANISM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS Beasley, E.M., Wei, M.H., Bonazzi, V.R., Sanders, R.C. and di Francesco, V.C. TITLE ISOlated human kinase proteins, nucleic acid molecules encoding	human Xinase proteins, and uses thereof bugan Xinase proteins, and uses thereof JOURNAL Patent: WO 0224920-A 1 28-MAR-2002; PE Corporation (NY) (US) FEATURES Location/Qualifiers 1. 2190 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" ORIGIN Query Match 100.0%; Score 1515; DB 6; Length 2190; Best Local Similarity 100.0%; Pred. No. 0; Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 ATGGAGGGGGTCCAGGTCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGCTG 60
FEATURES Location/Qualifiers 12190 / Organism="unknown" /mol_type="genomic DNA" ORIGIN Query Match 100.0%; Score 1515; DB 6; Length 2190; Best Local Similarity 100.0%; Pred. No. 0; Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 ATGAAGGGGTCCAGCTGTCTGCCAGGATCCTCGGGCAGAAGCGGTG 60 Db 173 ATGGAGGGGTCCAGCTGTCTGCCAGGATCCTCGGCAGAGCTGGTAGAACGGGTG 232 Qy 61 GCAGCCATCGATGACTCACTTGGAGGAGGCAGATGGTGGCCCAGAGCTACTAGAAAC 120 Db 233 GCAGCCATCGATGATGATGATGATGGTGGCCCAGAGCCTACTAGAAAC 292	Oy 121 GGTGTGGACCCCCCCACCACGGGCCAGAGTGCCTCTGTGATCCCTGGCAGTACTTCAAGA 180 Db 293 GGTGTGGACCCCCCCCCCACCAGGGCCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA 352 Qy 181 CTGCTCCCAGCCGGCCTAGCCTCTCAGCCAGAAGCTTTCCCTACAGAGCGCCAGCA 240 Db 353 CTGCTCCCAGCCTAGCCTCTCAGCCAGAAGCTTTCCCTACAGGAGCGCCAGCA 412 Cy 241 GGAAGCTATCTGGAGCGCTAGCCTTCAGCCAGGAGCCTTCCCTACAGGAGCCCAGCCATCTCC Qy 241 GGAAGCTATCTGGAGCGCAGGCTGGCCTTTCCCTACAGGAGCCCATCTCC	00 00 00 00 00 00 00 0	QY 481 AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCCCCCCGGAGAGGTCCCAG 540 Db 653 AAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCGGAGAGGTCCCAG 712 QY 541 GCTGCCAGGGAGGACCAGCAAGCAGCTGCTGCCCTCGCAGGAGTTACCAGGAGTT 600 T13 GCTGCCCAGGAGGACCAGCAAGCAGCTGCTGCCCTTGGAGCGGTTACCAGGAGTT 772 QY 601 GCCATCCTGAAGAAGCTGGACCAGCTGCTGCAGCTGATCGAGGTCCTGGATGAC 60 Db 773 GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC 83 QY 601 GCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC 83 CCAGCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGGAAACTGGATGAC 83 CCAGCTGAAGAACTCTAATTTGGTGTTTGACCTCCTGAAAAAGGGCCCGTCAAGGAA 892 Bb 833 CCAGCTCAAGAACTCTAATTTGGTGTTTGACCTCCTGAAAAAGGGCCCGTCAAGGAA 892	QY 721 GTGCCCTGTGACAAGCCCTTCTCGGAGGAAGCTCGCCTCTACCTGCGGGACGTCATC 780 Db 893 GTGCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTCATC 952 QY 781 CTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGACATCAAGCCATCCAAC 840 Db 953 CTGGGCCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAGGAGCATCAAGCATCCAAC 1012 QY 841 CTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT 900 Db 1013 CTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT 1072 QY 901 GAGGGGAACGTCAGCTGTCCAGCAGCGGGAACCCCAGCATTCATGGCCCCCCAGG 960 V 1073 GAGGGAACGTCAGCTGCCCGCGGGGAACCCCAGCATTCATGGCCCCCCGAG 1132 *Db 1073 GAGGGAACGTCCAGGCTCAGCTGCCCGGGGAACCCCAGCATTCATGGCCCCCCGAG 1132

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173 ATGGAGGGGCCCAGCTGCTGCTGCCAGGATCTCGGGCAGAGCTGGTAGAACGGTG 232 61 GCAGCCATCGATGTGACTCACTTCGAGGAGGCAATGGTGGCCCAGAGCCTACTAGAAC 120 61 GCAGCCATCGATGTGACTCACTTCGAGGAGGCCAGTGGCCCCAGAGCCTACTAGAAAC 120 62 GCAGCCATCGATGTGACTCACTTCGAGGGCCAGAGCCTACTAGAAAC 292 63 GCAGCCATCGATGTGACTCACTTGAGGGGCCAGAGCTTCAAGA 180 64 GCAGCCACCACCACCACCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGA 180 65 GCAGCACCCCCACCACGGGCCAGAGCTCTCTGATGATCCCTGGCAGTACTTCAAGA 352 66 GTGGGACCCCCACCACGGGCCAGAGCTTCCCTGGCAGAGCGCAGAGA 352 67 GCTCCCCAGCCCGGCCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGGGCCAGCA 412 66 GCTCCCCAGCCCGGCCCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGGGCCAGGA 412 67 GCTCCCCAGCCCGGCCCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGCCAGCA 412		

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GCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC
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I (bases I to 3538; Harvey, M. and Barden, N.
Tascedda, F., Carra, S., Harvey, M. and Barden, N.
Characterization of human CaMKK alpha gene structure
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Homo sapiens CaMKK alpha protein mRNA, complete cds.
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Tascedda,F., Carra,S., Harvey,M. and Bar
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Location/Qualifiers
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KSMLRKRSFGNPFEPQARREERSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS"
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0
                                                                                   Length 3529
                                                                                                                   2; Indels
                                                                                   DB 9;
                                                                                   Score 1511.8;
Pred. No. 0;
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Matches 1513;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
E. 1 (Bases I to 3575)
Strausberg, R.L. Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhar, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schectr, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Homo sapiens calcium/calmodulin-dependent protein kinase kinase 1, alpha, transcript variant 1, mRNA (cDNA clone MGC:49844

MAGE:551570), complete cds.
                         942 CTGCTCCTGGGGATGATGGGCCACGTGAAGATCGCCGACTTTGGCGTCAGCAACCAGTTT
                                                                                                1002 GAGGGGAACGACGCTCAGCTGTCCAGCACGGCGGGAACCCCAGCATTCATGGCCCCCGAG
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/db_xref="G1:23499314"
/tanslation="MEGGPACCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDP
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DWATGVTLXCFVYGKCPFIDDFILALHRKIKNEPVVPPEEPPISEELKDLILKMLDK
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KSMLRKRSFGNPFEPQARREERSMSAPGNLLVKEGFGGGGKSPELPGVQEDEAAS"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27437009. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susama Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Dannes Gmailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y. Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (109-704-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/clone_lib="NIH MGC 115"
/lab host="Plug"
/lab host="Plug"
/lab host="Pector: pCMV-SPORT6"
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/db_xref="LocusID:84254"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                         human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="calcium/calmodulin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/protein_id="AAH43487.1"
/db_xref="G1:27694084"
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AUTHORS
TITLE
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Braunschweig/Germany) within the CDNA sequencing consortium of the German Genome Project.
This clone is available at the RZDD in Berlin.
Please contact the RZDD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY, Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/CDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MEGGPAVCCQDPRAELVERVAAIDVTHLEEADGGPEPTRNGVDP
PPRARAASVIPGSTSRLLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPR
AWRRPTIESHHVAISDAEDCVQLNQYKLQSEIGKGAYGVVRLAYNESEDRHYAMKVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVL
DDABDNLYTVTVPULLAKQPYNEVPCIPKFSEEQSARLYIEDVILGLEYTHQGYTYHDI
KPSNLLLGDDGHVKLADFGYSVQPESNDAQLSSTAGTPAFWAPEAISDSGQSFSGKAL
DVWATGVTLYCFVYGKCPFIDDFILALHRKIKNEPVVPPEEPBISEELKOLILEKNLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPETRIGVPDIKLHPWVTKNGEEPLPSEEEHCSVVEVTEEEVKNSVRLIPSWTTVILV
KSMLRKRSFGNPFEPQARREERSMSAPGNLLVKEGFGEGGKSPELPGVQEDEAAS"
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCCGGGCCTGGCGGAGGCCCACCATCGAGTCCCACGTGGCCATCTCAGATGCAGAG 360
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/clone_lib="761 (synonym: hamy2). Vector pSportl;
DH10B; sites Not1 + Sal1"
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                                                                                                                                                                                                                   /organism="Homo sapiens"
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/db_xref="taxon:9606"
/map="26.0 cm from top of Chrl7 linkage
/clone="DKFZp761M0423"
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/db_xref="GI:13276655"
/db_xref="GOA:Q9BQH3"
/db_xref="SPTERMBL:Q9BQH3"
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="DXFZp761M0423"
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gene="DKFZp761M0423"
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                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
1. .3583
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Best Local Similarity 99.9
Matches 1513; Conservative
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wiemann, S., Weil, B., Wellenreuther, R., Gassenhuber, J., Glassl, S., Ansorge, W., Boecher, M., Bloecker, H., Bauersachs, S., Blum, H., Lauber, J., Duesterhoeft, A., Beyer, A., Kochrer, K., Strack, N., Mewes, H.W., Outenwaelder, B., Obermaier, B., Tampe, J., Heubner, D., Wambutt, R., Korn, B., Klein, M. and Poustka, A. Toward a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs Genome Res. 11 (3), 422-435 (2001)
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Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                           CTCCACAGGAAGATCAAGAATGAGCCCGTGGTGTTTCCTGAGGAGCCAGAAATCAGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCCCCAGCTGGACCACGTGATCCTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGG
                                                                                                         GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCATCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCCGTTTGAGCCCCCAGGAGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTA
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                        GCCATITICIGATICCGGCCAGAGCITCAGIGGAAGGCCTIGGAIGIAIGGGCCACIGGC
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Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens mRNA; cDNA complete cds.
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AUTHORS
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RESULT 8 AX455763 LOCUS DEPINITION Sequence 9 fro ACCESSION AX455763 VERSION AX455763 VERYWORDS SOURCE HOMO Sapiens ORGANISM HOMO Sapiens Mammalia; Euth REFERENCE AUTHORS MAMMALIA; BUTH REFERENCE AUTHORS TITLIE TITL	QUERY MATCh QUERY MATCh QUERY MATCh	Best Local Similarity Matches 1496; Conservat Qy	Db 61 GCAGCCATCGAT Qy 121 GCTGTGGACCCC Db 121 GGTGTGGACCCC Oy 181 CTGCTCCGAGCC	Db 181	Oy 361 GACTGCGTGCAG	
485 GTGGTGAGGCTGAACGAAAGTGAAGACACACTATGCAAAGTCCTTTCC 544 481 AAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCGGAGAGGTCCCAG 540 [GEGCCTGTGACAACCCTTCTGGAGGAGCAAGCTCGCTTACCTGCGGGACGTCATCGAAAGCGCCTGTGACATCGAAAGCTCGCCTTTTGACTTTGACTTCTGAGGAACGTCGCCTTTTTTTT	905 CTGCTCCTGGGGGATGATGGGCACGTGAAGATCGCCCACTTTGGCGTCAGCAGCTTT 900 905 CTGCTCCTGGGGGATGATGGCCACGTGAAGATCGCCGTCAGCAGCTTT 964 901 GAGGGGAACGACGCAGGAGGCAGCAGGAACCCCAGGATTT 964 901 GAGGGGAACGACGACGACGAGCAGCAGGAACCCCAGGATTCATGGCCCCCGAG 960	GCCATTCTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGCCACTGGCCGGCC	1145 CTCCACAGGAAGATGAGCCCGTGGTGTTTCCTGAGGAGATCAGCGAG 1140 1145 CTCCACAGGAAGATCAGCGAG 1140 1145 CTCCACAGGAAGATCAGGGAGTGTTTCCTGAGCGAGCCCAGAAATCAGCGAG 1204 1141 GAGCTCAAGGACCTGATCCTGAAGATTCCTGAGAATCCCGAGAATTGGGGTG 1204 1205 GAGCTCAAGGACCTGATCCTGAAGATTCCCGAGAATTGGGGTG 1206	1261 GAGGAGCACTGCAGCGTGGTGAGAGGGGGGGGGGGGGGG	1381 AACCCGTTTGAGCCCCAGGCACGGAGGGATCCATGTCTGCTCCAGGAACCTA 1440

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heria; Primates; Catarrhini; Hominidae; Homo.
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and 16002, novel human kinases and uses therefor 220800-A 9 14-MAR-2002;
ARM INC (US)
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Pred. No. 9.6e-312;
0; Mismatches 9; Indels 0;
 linear
 DNA
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ganism="Homo sapiens"
Lype="unassigned DNA"
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Pred. No. 9.1e-312;
0; Mismatches 9; Indels 0;
Meyers,R.A. and Silos-Santiago,I.
1658, 14223, and 16002, novel human kinases and Patent: WO 0220800-A 7 14-MAR-2002;
MILLENNIUM PHARM INC (US)
                                                                                                                                                                                                                                           'note="unnamed protein product"
                                                                                                                                         /organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
1987. 1883
                                                                                            Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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REFERENCE 1 AUTHORS PI. TITLE NO JOURNAL PA SOURCE SOURCE	Query Match Best Local S: Matches 1510	Qy 1	Qy 61	Qy 121 Db 121	Qy 181 Db 181	Qy 241	Qy 301 Db 301	Qy 361	Qy 407	Qy 454	Oy 514	QY 574 (Db 601 (Db 661 QY 694 Q	Db 718 (Qy 754 G
		901 GAGGGAACGACGCTCAGCTGTCCAGCACGGGGAACCCCAGCATTCATGGCCCCCGAG 960 	961 GCCAITICTGAITCCGGCCAGAGCTICAGTGGGAAGGCCTTGGAIGTAIGGGCCACTGGC 1020 	1021 GTCACGTTGTTTGTCTATGGGAAGTGCCCATTCATCGACGATTTCATCGGCC 1080	1081 CTCCACAGGAAGATCAAGAATGAGCCGTGGTGTTTCCTGAGGAGCCAGAAATCAGCGAG 1140 	1141 GAGCTCAAGGACCTGAACCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATTGGGGTG 1200 	1201 CCAGACATCAAGTTGCACCCTTGGGTGACCAAGAAGGGGGAGGAGCCCCTTCCTT	1261 GAGGACACTGCAGCGTGGTGGAGGTGACAGAGGGGGGGGTTAAGAACTCAGTCAG	1321 ATCCCCAGCTGCACGAGGTGATCCTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGG 1380	1381 AACCCGTTTGAGCCCCAGGGACGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTA 1440 	1441 CTGGTGAAAGAGGTTTGGTGAAGGGGCAAGAGCCCAGAGCTCCCCGGCGTCCAGGAA 1500 	GACGA 1505	1698 TACCA 1702	T 10 519	LOCUS AX166519 1542 bp DNA linear PAT 22-JUN-2001 DEFINITION Sequence 10 from Patent W00138503. ACCESSION AX166519	AX166519.1 G	URCE Homo sapiens (human) ORGANISM Homo sapiens Firearvots Montages
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llowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R., lanagan, P. and Clary, D.S. ovel human protein kinases and protein kinase-like enzymes attent: WO 0138503-A 10 31-MAY-2001;
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ammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                             96.3%; Score 1458.8; DB 6; Length 1542; llarity 97.9%; Pred. No. 7.2e-305; Conservative 0; Mismatches 2; Indels 30;
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                                                                                                          1. .1542
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xxef="taxon:9606"
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               Score 1457.2; DB 6,
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0; Mismatches 3;
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Human kinases
Patent: WO 0146397-A 14 28-JUN-2001;
Incyte Genomics, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                    GAGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTGGACCACGGTGATCCTGGTGAAG
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                                                   GCCGACTITGGCGTCAGCAACCAGTTTGAGGGGAACGACGCTCAGCTGTCCAGCACGGCG
                                                              GGAACCCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTTCAGTGGG
                                                                                                        GGAACCCCAGCATTCATGGCCCCCCGAGGCCATTCTGATTCCGGCCAGAGCTTCAGTGGG
                                                                                                                                      AAGGCCTTGGATGTATGGGCCACTGGCGTCACGTTGTACTGCTTTGTATGGGAAGTGC
                                                                                                                                                 CCATTCATCGACGATTTCATCCTGGCCCTCCACAGGAAGATCAAGAATGAGCCCGTGGTG
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Catarrhini; Hominidae;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/note="Incyte ID No: 2041716CB1"
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Sequence 14 from Patent WO0146397.
AX179641
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Mammalia; Eutheria; Primates;
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   Location/Qualifiers
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Clone distribution: MGC clone distribution information can be found
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KKKLLKQYGFPRRPPPRGSQAAQGGPAKQLLPLERVYQEIAILKKLDHVNVVKLIEVL
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MEVPCDRFFSBEQARTVVLIGLEYTHCQKLYHRDIKPSNILLGDDGHVKIADFGV
SNQFEGNDAQLSSTAGTPAFNA.PEALSDSGQSFSGKALDVWATGVTLYCFVYGKCPY
DDFILALHRKIKNEPVVFPEGPEISBELKOLILKMLDKNPFTRIGVPDIKLHPWVTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 51 Row: 1 Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 27437010.
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PPRARAASVIPGSTSRLLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPR
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                                                                                                              Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGAGGGGGTCCAGCTGCTGCTGCCAGGATCCTCGGGCAGAGCTGGTAGAACGGGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="Brain, Lung, Testis, adult, pooled whole"
/clone lib="NIH MGC_115"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="calcium/calmodulin-dependent protein kinase
alpha, isoform b"
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                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CAMKK1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Best Local Similarity 92.0°
Matches 1453; Conservative
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                          PUBMED
REFERENCE
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JOURNAL
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1. (bases 1 to 2469)

2. Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Rlausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Alteschul, S.F., Zeeberg, B. Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sannchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfact, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalsku, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length
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                 AAGGCCTTGGATGTATGGGCCACTGGCGTCATGTACTGCTTTGTCTATGGGAAGTGC 1053
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                                                                                                                                                                       TTTCCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGAC 1173
                                                                                                                                                                                                                                                                                      1202 TTTCCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTTAGAC 1261
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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BC031647.1 GI:21594835
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SOURCE

TITLE

Oy 1027 TTGTACTGCTTTGTCTA Db 1223 TTGTACTGCTTTGTCTA OY 1087 AGGAAGATCAAGAATGA Db 1283 AGGAAGATCAAGAATGA OY 1147 AAGGACCTGATCCTGAA OY 1207 ATCAAGTTGCACCTTG Db 1403 ATCAAGTTGCACCCTTG Db 1463 ACCTGCAGCGTGGTGGA OY 1267 CACTGCAGCGTGGTGGA OY 1327 AGCTGGACCTGGTGGA OY 1327 AGCTGGACCAGGTGGTGGA OY 1327 AGCTGGACCAGGTGGTGGA OY 1327 AGCTGGACCAGGTGGTGGA OY 1387 TTTGAGCCCCAGGTGATA OY 1387 TTTGAGCCCCAGGTGATG Db 1523 AGCTGGACCCAGGTGGTGA OY 1387 TTTGAGCCCCCAGGTGATG Db 1583 TTTGAGCCCCCAGGTGATG Db 1583 TTTGAGCCCCCAGGCACG OY 1447 AAAGAAGGGTTTGGTGG	RESULT 13 BC017529 BC017529 BC017529 LOCUS MUS musculus calciu alpha, mRNA (CDNA or CONTROLY) REVENCION RCT MUS musculus (Nouse ONGANISM MUS musculus (Nouse ONGANISM MUS musculus (Nouse ONGANISM MUS musculus (Nouse ONGANISM MUS musculus (Nouse ONGANISM MUS musculus (Nouse ONGANISM MUS musculus (Nouse ONGANISM) MUSCULUS (Nouse ONGANISM) AUTHORS Straubberg, R.L., Pernoge Carninci, P., Parnoge Carninci, P., Multing Carninci, P., Multing Bouffard, G.G., Blak Dickson, M.C., Rodri Butterfield, Y.S., K. MUDLINE SARRENCE MEDELINE 22388257 MUTHORS Straubberg, R. MUTHORS Straubberg, R. MUTHORS Straubberg, R. MUTHORS Straubberg, R. MUTHORS Straubberg, R. MUTHORS Straubberg, R. MUTHORS TITLE Direct Submission JOURNAL Direct Submission JOURNAL DIRECT SUBMISSION JOURNAL DIRECT SUBMISSION JOURNAL DIRECT SUBMISSION JOURNAL DIRECT SUBMISSION JOURNAL JO
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                                                                                                   CTGCTCCCAGCCCGGCCTTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGCCAGCA
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PWRRPTISERWAISOTEDCYOLNOYKLOSEIGKGAYGVRLAYNESEDRHYAMKULS
KKKLLKQYGFPRRPTASOTEDCYOLNOYKLOSEIGKGAYGVVRLAYNESEDRHYAMKULS
BDPAEDNLYLVPDLERKGPWRPYCDKFFPEDGARLYLRDIILGLEYLHCOKIVHRDI
BVAEDNLYLVPDLERKGPWRPYCDKFFPEDGARLYLRDIILGLEYLHCOKIVHRDI
BVATGVTLYCFVYGKCPFPIDDYILTHRKINNEAVVFPEDEBEDRSEDLENDLILKDLIKMLDK
NPETRIGOSOTKLHWYTKGREPLESEEETGSVVEVTEBEVKRDIFEDLILTHRINDK
KSMLRKRSFGNPFEPOARRERSMSAPGSLLMKEGGGGGCKSPELPGCYQEDEAAS"
                                                                                                                                                                                                                   Info@bogsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MESGPAVCCQDPRAELVDRVAAINVAHLEEADEGPEPARNGVDP"
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/strain=FVB/N"
/db_xref="tracn:10090"
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/tlssue type="Ralivary gland, 10 week old female mouse"
/clone lib="NGI CGAP_SG2"
/lab_host="HHOB"
Cancer Genomics Office, National Cancer
rive. Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="%_TKc; Region: Serine/Threonine protein kinases,
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                                                                              Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Itssue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
E. Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.9%; Score 1241.4; DB 10; Length 3435;
88.7%; Pred. No. 6.7e-258;
iive 0; Mismatches 171; Indels 0;
                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                George Yang, Scott Zuyderduyn, Marco Marra.
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      Collection (MGC), Cancer Genomics C. tute, 31 Center Drive, Room 11A03,
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db_xref="LocusID:55984"
db_xref="MGI:1891766"
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KPSNLLLGDDGHVKIADFGVSNQFEGNDAOLSSTAGTPAFMAPEAISDTGQSFSGKAL
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NPETRIGVSDIKLHPWVTKHGEEPLPSEEEHCSVVEVTEEEVKNSVKLIPSWTTVILV
KSMLRKRSFGNPFEPQARREERSMSAPGNLLLKEGGGEGGKSPELPGVQEDEAAS"
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                                                                                                Length 3429,
                                                                                              Score 1238.2; DB 10; Lengt
Pred. No. 3.3e-257;
Mismatches 173; Indels
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ilarity 88.6%;
Conservative (
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Matches 1342;
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PPRARAASVIPGSASRPTPVRPSLSARKFSLQBRPAGSCLEAGVGPVSTGPASHASPR
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KKKLLKQYGPPRRPPRGSQAPQGGPAKQLLPLERVYQBIALLKKLDHVNVVKLIBUL
DDPAEDNLYLVPDLLRKGPWMEVPCDKPFPEBQARLYLRDIILGLEYLHCQKIVHRDI
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Sciurognathi, Muridae, Murinae,
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Okuno,S., Kitani,T. and Fujisawa,H.
Bvidence for the existence of Ca2+/calmodulin-dependent protein
kinase IV kinase isoforms in rat brain
J. Blochem. 119 (6), 1176-1181 (1996)
96425044
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            GACCTCAAAGACCTGATCCTGAGGATGCTAGACAAGAATCCTGAGACAAGAATTGGGGGTG
                                           ATCCCCAGCTGGACCACGGTGATCCTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGG
                                                                                                                                                                                                                               AACCCGTTTGAGCCCCCAGGCACGGAGGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTA
                                                                                                                                                                                                                                                          AACCCATTCGAGCCCCAAGCACGCAGGAAGAAGAACATCCATGTCTGCACCAGGAAGCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenBank staff at the National Library of Medicine created thi entry [NCBI gibbsq 179633] from the original journal article. This sequence comes from Fig. 1.

Location/Qualifiers
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'/gene="Ca2+/calmodulin-dependent protein kinase IV isoform, CaM-kinase kinase alpha"
107. .1624
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/product="Ca2+/calmodulin-dependent
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/db_xref="GI:1836161"
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/db_xref="taxon:10118"
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Mammalia; Eutheria; Rodentia;
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GATGAGGCTGCGTCC 1641
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AUTHORS
TITLE
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alpha, CaM-kinase kinase alpha"
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/db xref="G1:4512334"
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                                                                                                                                                                                                                                                            DDPAEDMLYLVFDLLRKGPVMEVPCDKPFPEEQARLYLRDIILGLEYLHCQKIVHRDI
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DVWAPIGVILYCFVVGKCPFTDBYILALHRKIRGNEAVVPPEEPRVSEELKDLILEKHLDK
NPETRIGVSDIKLHPWVTKHGBEPLPSEEEHCSVVEVTEEEVKASVKLIPSWITTVILA
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                                                                       107. 1524
/codon_start=1
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Pred. No. 7.4e-257;
0; Mismatches 174; Indels
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/tissue_lib="brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                           /note="18 a nucleotides"
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Best Local Similarity 88.5%;
Matches 1341; Conservative
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Rattus norvegicus mRNA for Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha, complete cds.
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Ca/calmodulin-dependent protein kinase kinase alpha, CaM-kinase
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Evidence for the existence of Ca2+/calmodulin-dependent protein kinase IV kinase isoforms in rat brain
J. Blochem. 119 (6), 1176-1181 (1996)
                                                                                                              | GAGCTCAAGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGAGACGAGAGTGGGGGTG
               GCCATTICTGATTCCGGCCAGAGCTTCAGTGGGAAGGCCTTGGATGTATGGGCCACTGGC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pujisawa, H. and Okuno, S.
Direct Submission
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